

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: June 20, 2001, 16:52:04 ; Search time 187.07 Seconds
(without alignments)
9748.932 Million cell updates/sec

Title: US-09-464-377-1

Perfect score: 3124
Sequence: 1 agggggccttgagccggacc.....taaaagtgttgccttgtaa 3124

Scoring table:
IDENTITY-NUC
Gapop 10.0, Gapext 1.0

Searched: 678276 seqs, 291890651 residues

Total number of hits satisfying chosen parameters: 1356552

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

N.Geneseq.0401.*
1: /SIDS2/gcgdata/geneseq/geneseq/NA1980.DAT.*
2: /SIDS2/gcgdata/geneseq/geneseq/NA1981.DAT.*
3: /SIDS2/gcgdata/geneseq/geneseq/NA1982.DAT.*
4: /SIDS2/gcgdata/geneseq/geneseq/NA1983.DAT.*
5: /SIDS2/gcgdata/geneseq/geneseq/NA1984.DAT.*
6: /SIDS2/gcgdata/geneseq/geneseq/NA1985.DAT.*
7: /SIDS2/gcgdata/geneseq/geneseq/NA1986.DAT.*
8: /SIDS2/gcgdata/geneseq/geneseq/NA1987.DAT.*
9: /SIDS2/gcgdata/geneseq/geneseq/NA1988.DAT.*
10: /SIDS2/gcgdata/geneseq/geneseq/NA1989.DAT.*
11: /SIDS2/gcgdata/geneseq/geneseq/NA1990.DAT.*
12: /SIDS2/gcgdata/geneseq/geneseq/NA1991.DAT.*
13: /SIDS2/gcgdata/geneseq/geneseq/NA1992.DAT.*
14: /SIDS2/gcgdata/geneseq/geneseq/NA1993.DAT.*
15: /SIDS2/gcgdata/geneseq/geneseq/NA1994.DAT.*
16: /SIDS2/gcgdata/geneseq/geneseq/NA1995.DAT.*
17: /SIDS2/gcgdata/geneseq/geneseq/NA1996.DAT.*
18: /SIDS2/gcgdata/geneseq/geneseq/NA1997.DAT.*
19: /SIDS2/gcgdata/geneseq/geneseq/NA1998.DAT.*
20: /SIDS2/gcgdata/geneseq/geneseq/NA1999.DAT.*
21: /SIDS2/gcgdata/geneseq/geneseq/NA2000.DAT.*
22: /SIDS2/gcgdata/geneseq/geneseq/NA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1594	51.0	4310	21	C77525 Human ORFX ORF3080
2	1478	47.3	2223	21	Z46024 Human encoding a hu
3	493	15.8	621	21	Z46042 Partial cDNA encod
4	443	14.2	549	21	Z46043 Partial cDNA encod
5	420	13.4	647	21	Z46044 Partial cDNA encod
6	407.2	13.0	504	20	V88444 EST clone G128. H
7	284.2	9.1	631	21	Z46041 Partial cDNA encod
8	222.2	7.1	258	21	Z46040 Partial cDNA encod
9	221.4	7.1	256	21	Z46039 Partial cDNA encod
10	203.6	6.5	300	21	A00854 Human colon cancer
11	193.8	6.2	1005	20	X20438 Human secreted pro

12	139.8	4.5	529	21	Z46046
13	123.2	3.9	217	14	Q61313
14	116.8	3.7	578	21	C69663
15	116.8	3.7	1308	19	V44275
16	116.8	3.7	1349	20	Z33652
17	116.8	3.7	1349	21	C77734
18	107.8	3.5	220	21	Z46047
19	106.6	3.4	655	21	Z46045
20	106.2	3.4	796	21	F07636
21	104.2	3.3	1167	21	C42338
22	94.4	3.0	1867	21	A12404
23	89.8	2.9	1437	21	C40487
24	73.2	2.3	380	21	C76228
25	72.2	2.3	392	21	C02002
26	70.2	2.2	579	18	X83336
27	70.2	2.2	579	19	V68878
28	70.2	2.2	579	21	C80859
29	48.6	2.2	579	21	Q27091
30	48.4	1.6	1028	13	Q09010
31	48.4	1.5	1272	21	A29006
32	48.4	1.5	4524	20	V33912
33	47.2	1.5	114955	20	X53491
34	46	1.5	114955	20	X53491
35	45.4	1.5	1655	21	Z61589
36	45.4	1.5	1655	21	Z61592
37	45.2	1.4	6002	20	X60227
38	45	1.4	530	21	A95215
39	44.6	1.4	3765	13	Q31890
40	43.8	1.4	1266	20	X09011
41	43.8	1.4	1266	21	A29007
42	43.4	1.4	4475	14	A45995
43	43.2	1.4	6728	21	Z35248
44	43.2	1.4	26338	19	V62134
45	43.2	1.4	133719	21	C64754

ALIGNMENTS

RESULT 1

C77525
ID C77525 standard; cDNA; 4310 BP.

AC C77525;

DT 08-FEB-2001 (first entry)

DE Human ORFX ORF3080 polynucleotide sequence SEQ ID NO:6159.

Human; open reading frame; ORFX; detection; cytostatic; hepatotropic;
vulnerable; antiproliferative; antiparkinsonian; neurotrophic; neuroprotective;
anticonvulsant; osteopathic; antidiarrheal; immunosuppressant; cardiant;
immunostimulant; thrombolytic; coagulant; vasotropic; antidiabetic;
hypocensative; dermatological; immunosuppressive; antineoplastic;
antiviral; antibacterial; antifungal; antineoplastic; antithyroid;
antianaemic; gene therapy; cancer; proliferative disorder; hypertension;
neurodegenerative disorder; osteoarthritis; graft vs host disease;
cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS;
cholesterol ester storage; systemic lupus erythematosus; infection;
severe combined immunodeficiency; malaria; autoimmune disorder; asthma;
allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound;
bone damage; cartilage damage; antiinflammatory disease; coagulation;
thrombosis; contraceptive; ss.

OS Homo sapiens.

PN WO200058473-A2.

PD 05-OCT-2000.

PF 31-MAR-2000; 2000WO-US08621.

PR 31-MAR-1999; 99US-0127607.

Partial cDNA encod
Human Brain, Expres
Human arginine met
Human interferon r
Human breast tumor
Human cancer assoc
Partial cDNA encod
Partial cDNA encod
Fusarium venenatum
Arabidopsis thalia
cDNA encoding a hu
Arabidopsis thalia
Human ORFX ORF783
Human secreted pro
Breast cancer tumor
DNA molecule encod
Human breast tumor
X7726 probe. Homo
Brn-3a polynucleot
Nucleotide sequenc
Human adenosine A1
Human adenosine A1
DNA encoding a hum
Poly(A) binding pr
Human OCT-1 part
FMR-1 gene for det
Brn-3a polynucleot
Murine transcript
IDUA - exons III t
Human BMP-2 gene 5
HSV-2 strain SB5 C
Macaca mulatta rha

[illegible]

KW	autoimmune thyroiditis; bronchitis; Crohn's disease; diabetes mellitus;
KM	gout; Grave's disease; osteoarthritis; osteoporosis; pancreatitis;
KM	psoriasis; rheumatoid arthritis; infection; neurological disorder;
KW	epilepsy; ischemic cerebrovascular disease; stroke; Alzheimer's disease;
KW	Pick's disease; Huntington's disease; dementia; Parkinson's disease;
KV	extrapyramidal disorder; viral central nervous system disease;
KW	pilon disease; central nervous system developmental disorder;
KW	neuroskeletal disorder; muscular dystrophy; neuromuscular disorder;
KV	peripheral nervous system disorder; mental disorder; schizophrenic;
KM	anxiety; reproductive disorder; gastrointestinal disorder; dyspepsia;
KM	indigestion; gastritis; anorexia; nausea; abdominal angina;
KW	gastroenteritis; intestinal obstruction; peptic ulcer;
KM	irritable bowel syndrome; diarrhoea; constipation;
KW	gastrointestinal haemorrhage; cancer; ss.
XX	
OS	Homo sapiens.
XX	
Key	Location/Qualifiers
FT	CDS 224..1566
FT	/tag= a
FT	/product= "transferase"
FT	/transl_except= (pos: 1100..1101, aa: Ala)
FT	224..361
FT	/tag= b
XX	
PN	WO200000594-A2.
PD	06-JAN-2000.
XX	
PF	29-JUN-1999; 99MO-US14651.
XX	
PR	30-JUN-1998; 98US-0109204.
XX	
PA	(INCY-) INCYTE PHARM INC.
PI	Lal P, Bandman O, Hillman JL, Guegler KJ, Gorgone GA, Corley NC;
PI	Patterson C;
DR	WP1: 2000-147267/13.
XX	
XX	P-PSDB: Y54593.
PT	Novel human transferases used for the diagnosis, treatment, and
PT	prevention of autoimmune/inflammatory, neurological, reproductive and
PS	gastrointestinal disorders and cancer
XX	
PS	Claim 7; Page 82; 95pp; English.
CC	
CC	The present sequence encodes a transferase polypeptide, designated
CC	HUTRAN-3. The HUTRAN cDNA sequence is derived from Incyte clone
CC	2555071. The sequence is obtained from the partial sequences 246039-47.
CC	The polypeptide is a arginine methyltransferase. The HUTRAN polypeptides
CC	polynucleotides, agonists, antagonists, and antibodies can be used to
CC	diagnose, treat or prevent autoimmune/inflammatory diseases (e.g. AIDS,
CC	adult respiratory distress syndrome, allergies, asthma, atherosclerosis,
CC	autoimmune thyroiditis, bronchitis, Crohn's disease, diabetes mellitus,
CC	gout, Grave's disease, osteoarthritis, osteoporosis, pancreatis,
CC	psoriasis, rheumatoid arthritis, infections, trauma, neurological
CC	disorders (e.g. epilepsy, ischemic cerebrovascular disease, stroke,
CC	Alzheimer's disease, Pick's disease, Huntington's disease, dementia,
CC	Parkinson's disease and other extrapyramidal disorders), viral central
CC	nervous system disease, pilon diseases, central nervous system
CC	developmental disorders, neuroskeletal disorders, muscular dystrophy,
CC	neuromuscular disorders, peripheral nervous system disorders, mental
CC	disorders, schizophrenic, anxiety, reproductive disorders and
CC	gastrointestinal disorders (e.g. dyspepsia, indigestion, gastritis,
CC	anorexia, nausea, abdominal angina, gastroenteritis, intestinal
CC	obstruction, intestinal tract infections, peptic ulcer, irritable bowel
CC	syndrome, diarrhoea, constipation, gastrointestinal haemorrhage, and
CC	cancer.
XX	
XQ	Sequence 2223BP; 465 A; 732 C; 580 G; 444 T; 2 other:

Query Match 47.3%; Score 1478; DB 21; Length 2223;
Best Local Similarity 82.6%; Pred. No. 0;
Matches 1892; Conservative 0; Mismatches 311; Indels 88; Gaps 14;

QY 230 cagatgcatgctgtgagcagacagctctctacacacccctggctgcaacagctc 349
Db 1 cagatgcatgctgtgagcagacagctctctacacacccctggctgcaacagctc 60
QY 350 tcatcagattgacacacccacagatt--ctgttcttctacacacccctgaaactg 407
Db 61 tcatcagattgacacacccacacagattcgtcagcttctacacacccctgaaactg 120
QY 408 tgggggacacacacacacacacacacacacacacacacacacacacacacac 467
Db 121 cgggggacacacacacacacacacacacacacacacacacacacacacacac 180
QY 468 gcaagatctcagcttctacacacacacacacacacacacacacacacacacac 527
Db 181 gcaagatctcagcttctacacacacacacacacacacacacacacacacacac 240
QY 528 gcgagacagacacacacacacacacacacacacacacacacacacacacacac 587
Db 241 gcgagacagacacacacacacacacacacacacacacacacacacacacacac 300
QY 588 cgttctagatgtggtggtggtggtggtggtggtggtggtggtggtggtggtggt 647
Db 301 cgttctagatgtggtggtggtggtggtggtggtggtggtggtggtggtggtggt 360
QY 648 caggaacacacacacacacacacacacacacacacacacacacacacacacac 707
Db 361 caggaacacacacacacacacacacacacacacacacacacacacacacacac 420
QY 708 gactaacacacacacacacacacacacacacacacacacacacacacacacac 767
Db 421 gactaacacacacacacacacacacacacacacacacacacacacacacacac 480
QY 768 gactaacacacacacacacacacacacacacacacacacacacacacacacac 827
Db 481 gactaacacacacacacacacacacacacacacacacacacacacacacacac 540
QY 828 aatgctcgaagctacacacacacacacacacacacacacacacacacacacac 887
Db 541 aatgctcgaagctacacacacacacacacacacacacacacacacacacacac 600
QY 888 caccacatgctgacacacacacacacacacacacacacacacacacacacac 947
Db 601 caccacatgctgacacacacacacacacacacacacacacacacacacacac 660
QY 948 caccacacacacacacacacacacacacacacacacacacacacacacacac 1007
Db 661 caccacacacacacacacacacacacacacacacacacacacacacacacac 720
QY 1008 aggtgacgctgtgagatgacacacacacacacacacacacacacacacacacac 1067
Db 721 aggtgacgctgtgagatgacacacacacacacacacacacacacacacacacac 780
QY 1068 cctgtgacgacacacacacacacacacacacacacacacacacacacacacac 1127
Db 781 cctgtgacgacacacacacacacacacacacacacacacacacacacacacac 840
QY 1128 gcaacagatagacacacacacacacacacacacacacacacacacacacacac 1187
Db 841 gcaacagatagacacacacacacacacacacacacacacacacacacacacac 900
QY 1188 ggccttcgttgcacacacacacacacacacacacacacacacacacacacacac 1247
Db 901 ggccttcgttgcacacacacacacacacacacacacacacacacacacacacac 960
QY 1248 ccccaacagacacacacacacacacacacacacacacacacacacacacacac 1307
Db 961 ccccaacagacacacacacacacacacacacacacacacacacacacacacac 1020
QY 1308 tgcacagcgccgggacacacacacacacacacacacacacacacacacacacac 1367

Db 1021 cgcacagcgccgggacacacacacacacacacacacacacacacacacacacac 1080
QY 1368 ctatgacatcagatgtgtgacacacacacacacacacacacacacacacacacacac 1427
Db 1081 ctatgacatcagatgtgtgacacacacacacacacacacacacacacacacacacac 1139
QY 1428 gcatcacaacacacacacacacacacacacacacacacacacacacacacacac 1487
Db 1140 gcatcacaacacacacacacacacacacacacacacacacacacacacacacac 1199
QY 1488 acacacacacacacacacacacacacacacacacacacacacacacacacacacac 1547
Db 1200 acacacacacacacacacacacacacacacacacacacacacacacacacacacac 1259
QY 1548 cggggtgctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1607
Db 1260 cggggtgctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1319
QY 1608 ctccagtggtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1667
Db 1320 ctccagtggtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1379
QY 1668 ccaatcccgatgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1727
Db 1380 ccaatcccgatgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1439
QY 1728 ggg--gagcgcggtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1784
Db 1440 gggcgagtggtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1499
QY 1785 tggcgctgcacacacacacacacacacacacacacacacacacacacacacacac 1844
Db 1500 tggcgctgcacacacacacacacacacacacacacacacacacacacacacacac 1559
QY 1845 gactgagtgctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1904
Db 1560 gactgagtgctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1607
QY 1905 agtcacagc--ccggacacacacacacacacacacacacacacacacacacacacac 1961
Db 1608 agtcacagc--ccggacacacacacacacacacacacacacacacacacacacacac 1665
QY 1962 caccgctgcacacacacacacacacacacacacacacacacacacacacacacac 2020
Db 1666 caccgctgcacacacacacacacacacacacacacacacacacacacacacacac 1725
QY 2021 ctgcccacacacacacacacacacacacacacacacacacacacacacacacacacac 2080
Db 1726 ctgcccacacacacacacacacacacacacacacacacacacacacacacacacacac 1782
QY 2081 acatgagatcctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 2138
Db 1783 acatgagatcctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1842
QY 2139 ctgtgacatcgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 2198
Db 1843 ctgtgacatcgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1892
QY 2199 gcaagagagcgacacacacacacacacacacacacacacacacacacacacacac 2258
Db 1893 gcaagagagcgacacacacacacacacacacacacacacacacacacacacacacac 1913
QY 2259 ttgacatccctcactgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 2318
Db 1914 ttgacatccctcactgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1973
QY 2319 ggcacatgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 2378
Db 1974 ggcacatgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 2031
QY 2379 agaacacagtgacacacacacacacacacacacacacacacacacacacacacacacac 2437

Db 2032 agaacagctgtcaatccgcagacacccctctgtgaagccagcgccgagccgagccagcag 2091
Qy 2438 cccctgttcttagcagccagag-ttctaggtgaggggtggcccttcaagccttcagagt 2496
Db 2092 cccctctccttagcagcagcgagcgagggtggcccgccgaggttcagg- 2150
Qy 2497 gggcagagccctccaccacaaaggttaccctcaacttgatgtacaaaccacccagct 2556
Db 2151 -----gccctcccnacaaactgttaccctcacacttgatgtacaaaccacccagct 2205
Qy 2557 gtccaagggc 2567
Db 2206 gtccggaaagc 2216

RESULT 3
ID 246042
AC 246042 standard; cDNA; 621 BP.
XX 246042;
XX 25-APR-2000 (first entry)
XX Partial cDNA encoding a transferase designated HUTRAN-3 fragment.
DE
XX Transferase; HUTRAN-3; arginine methyltransferase; autoimmune disorder;
XX inflammatory disorder; AIDS; atherosclerosis;
XX adult respiratory distress syndrome; allergy; asthma; trauma;
XX autoimmune thyroiditis; bronchitis; Crohn's disease; diabetes mellitus;
XX gout; Grave's disease; osteoarthritis; osteoporosis; pancreatitis;
XX psoriasis; rheumatoid arthritis; infection; neurological disorder;
XX epilepsy; ischemic cerebrovascular disease; stroke; Alzheimer's disease;
XX Pick's disease; Huntington's disease; dementia; Parkinson's disease;
XX extrapyramidal disorder; viral central nervous system disease;
XX prion disease; central nervous system developmental disorder;
XX neuroskeletal disorder; muscular dystrophy; neuromuscular disorder;
XX peripheral nervous system disorder; mental disorder; schizophrenia;
XX anxiety; reproductive disorder; gastrointestinal disorder; dyspepsia;
XX indigestion; gastritis; anorexia; nausea; abdominal angina;
XX gastroenteritis; intestinal obstruction; peptic ulcer;
XX irritable bowel syndrome; diarrhoea; constipation;
XX gastrointestinal haemorrhage; cancer; ss.
XX
XX Homo sapiens.
OS
XX WO200000594-A2.
XX
XX 06-JAN-2000.
XX
XX 29-JUN-1999; 99WO-US14651.
XX
XX 30-JUN-1998; 98US-0109204.
XX
XX (INCYTE) INCYTE PHARM INC.
XX
XX Lal P, Bandman O, Hillman JL, Guegler KJ, Gorgone GA, Corley NC;
PI Patterson C;
XX
XX WPI; 2000-147267/13.
XX
XX Novel human transferases used for the diagnosis, treatment, and
PT prevention of autoimmune/inflammatory, neurological, reproductive and
PT gastrointestinal disorders and cancer
XX
XX
XX Disclosure; Page 90; 95pp; English.
XX
XX 246039-47 represent partial fragments which were used to produce Incyte
CC clone 2525071, which encodes a transferase polypeptide, designated
CC HUTRAN-3. The polypeptide is an arginine methyltransferase. The
CC HUTRAN polypeptides, polynucleotides, agonists, antagonists, and
CC antibodies can be used to diagnose, treat or prevent autoimmune/
CC inflammatory diseases (e.g. AIDS, adult respiratory distress syndrome,
CC allergies, asthma, atherosclerosis, autoimmune thyroiditis, bronchitis,

CC Crohn's disease, diabetes mellitus, gout, Grave's disease,
CC osteoarthritis, osteoporosis, pancreatitis, psoriasis, rheumatoid
CC arthritis, infections, trauma, neurological disorders (e.g. epilepsy,
CC ischemic cerebrovascular disease, stroke, Alzheimer's disease, Pick's
CC disease, Huntington's disease, dementia, Parkinson's disease and other
CC extrapyramidal disorders, viral central nervous system disease, prion
CC diseases, central nervous system developmental disorders, neuroskeletal
CC disorders, muscular dystrophy, neuromuscular disorders, peripheral
CC nervous system disorders, mental disorders, schizophrenia, anxiety,
CC reproductive disorders and gastrointestinal disorders (e.g. dyspepsia,
CC indigestion, gastritis, anorexia, nausea, abdominal angina,
CC gastroenteritis, intestinal obstruction, intestinal tract infections,
CC peptic ulcer, irritable bowel syndrome, diarrhoea, constipation,
CC gastrointestinal haemorrhage, and cancer.
XX
XX Sequence 621 BP; 135 A; 180 C; 150 G; 140 T; 16 other;
SQ

Query Match 15.8%; Score 493; DB 21; Length 621;
Best Local Similarity 88.0%; Pred No. 1.7e-115;
Matches 529; Conservative 0; Mismatches 72; Indels 0; Gaps 0;

Qy 706 aagagtaacaatctgacagacgcatcgtgtgtatcccttgccaaagttagagagttca 765
Db 21 atgcmaattagacnccgagcccaacgctcctccgagcaggtggagagtgta 80
Qy 766 ttgcttgacagtggtgacattatcatctagaagccatgggtcatgcttcaatgaa 825
Db 81 cttcccgagcaggttgacatcatcatctcgtgacccatgggtcatcttcaacag 140
Qy 826 cgaatgctgagagctacatctcatgccaagaagttacttaagcttgtaaacatgctc 885
Db 141 cgcagctgganagctactctcaacgccaagaagttacttaagcagcggaacaagtct 200
Qy 886 ccacacattgtatgtccactcgaccccttcaactatgtaacagctctacatgagcag 945
Db 201 cctacattgtgagctgccacttgcaccccttcaacgagatgacagctctacatgagcag 260
Qy 946 ttccacaaagcgaacttcgagcagcagcatcttcacagagtgtagctgtgcctc 1005
Db 261 ttccacaaagcgaacttcgagcagcagcatcttcacagagtgtagctgtgcctc 320
Qy 1006 aagagtgccgctgtgagtagtacttcggaacccgtgtgtgacacattgacacccg 1065
Db 321 cgaggtgccgcntgmntntnttccggagcgtgtgtgtgacacattgacacccg 380
Qy 1066 atccgtatggccaatctgtcaagtaacagtgaaacttcttagaagccaaagagcgat 1125
Db 381 atccgtatggccaatctgtcaagtaacagtgaaacttcttagaagccaaagagat 440
Qy 1126 ttgcacagagataaatcccatcaatccacatgctcagtgatcaggtcagtgatgac 1185
Db 441 ttgcacagagataaatcccatcaatccacatgctcagtgatcaggtcagtgatgac 500
Qy 1186 ttggcctctgttgcagtgcttcatgttgccttcatatgaacgttggtatccaca 1245
Db 501 ctgagcttctgttgcagtgcttcatgttgccttcatatgaacgttggtatccaca 560
Qy 1246 gccccaagagccctgacccatgtaacagtgtaacagtgctgctctcagtcagtcag 1305
Db 561 gccccaagagccctgacccatgtaacagtgtaacagtgctgctctcagtcagtcag 620
Qy 1306 t 1306
Db 621 t 621

RESULT 4
ID 246043/c
AC 246043 standard; cDNA; 549 BP.
XX 246043;
XX

Db	302	ccagcagcgtggtctgtgtgaaggtacaaccctgaaggccgcgtggtatcc	361
Qy	743	ctggcaaatgaaggag	760
Db	362	cggggaagaatgaagg	379
RESULT	8		
ID	246040	standard; CDNA; 258 BP.	
XX	246040;		
XX	25-APR-2000	(first entry)	
DE	Partial cDNA encoding a transferase designated HUTRAN-3 fragment.		
XX	Transferase; HUTRAN-3; arginine methyltransferase; autoimmune disorder;		
XX	inflammatory disorder; AIDS; atherosclerosis;		
XX	adult respiratory distress syndrome; allergy; asthma; trauma;		
XX	autoimmune thyroiditis; bronchitis; Crohn's disease; diabetes mellitus;		
XX	gout; Grave's disease; osteoarthritis; osteoporosis; pancreatitis;		
XX	psoriasis; rheumatoid arthritis; infection; neurological disorder;		
XX	epilepsy; ischemic cerebrovascular disease; stroke; Alzheimer's disease;		
XX	Picks disease; Huntington's disease; dementia; Parkinson's disease;		
XX	extrapyramidal disorder; viral central nervous system disease;		
XX	pilon disease; central nervous system developmental disorder;		
XX	neuroskeletal disorder; muscular dystrophy; neuromuscular disorder;		
XX	peripheral nervous system disorder; mental disorder; schizophrenia;		
XX	anxiety; reproductive disorder; gastrointestinal disorder; dyspepsia;		
XX	indigestion; gastritis; anorexia; nausea; abdominal angina;		
XX	gastroenteritis; intestinal obstruction; peptic ulcer;		
XX	irritable bowel syndrome; diarrhoea; constipation;		
XX	gastrointestinal haemorrhage; cancer; ss.		
OS	Homo sapiens.		
XX	WO200000594-A2.		
XX	06-JAN-2000.		
XX	29-JUN-1999;	99WO-US14651.	
XX	30-JUN-1998;	98US-0109204.	
XX	(INCYTE -) INCYTE PHARM INC.		
XX	Lal P, Bandman O, Hillman JL, Guegler KJ, Gorgone GA, Corley NC;		
XX	Patterson C;		
XX	WPI; 2000-147267/13.		
XX	Novel human transferases used for the diagnosis, treatment, and		
XX	prevention of autoimmune/inflammatory, neurological, reproductive and		
XX	gastrointestinal disorders and cancer		
XX	Disclosure; Page 89; 95pp; English.		
XX	246039-47 represent partial fragments which were used to produce Incyte		
XX	clone 2525071, which encodes a transferase polypeptide, designated		
XX	HUTRAN-3. The polypeptide is an arginine methyltransferase. The		
XX	HUTRAN polypeptides, polynucleotides, agonists, antagonists, and		
XX	antibodies can be used to diagnose, treat or prevent autoimmune/		
XX	inflammatory diseases (e.g. AIDS, adult respiratory distress syndrome,		
XX	allergies, asthma, atherosclerosis, autoimmune thyroiditis, bronchitis,		
XX	Crohn's disease, diabetes mellitus, gout, Grave's disease,		
XX	osteoarthritis, osteoporosis, pancreatitis, psoriasis, rheumatoid		
XX	arthritis, infections, trauma, neurological disorders (e.g. epilepsy,		
XX	ischemic cerebrovascular disease, stroke, Alzheimer's disease, Picks		
XX	disease, Huntington's disease, dementia, Parkinson's disease and other		
XX	extrapyramidal disorders, viral central nervous system disease, pilon		
XX	diseases, central nervous system developmental disorders, neuroskeletal		

CC	disorders; muscular dystrophy, neuromuscular disorders, peripheral
CC	nervous system disorders, mental disorders, schizophrenia, anxiety,
CC	reproductive disorders and gastrointestinal disorders (e.g. dyspepsia,
CC	indigestion, gastritis, anorexia, nausea, abdominal angina,
CC	gastroenteritis, intestinal obstruction, intestinal tract infections,
CC	peptic ulcer, irritable bowel syndrome, diarrhoea, constipation,
CC	gastrointestinal haemorrhage, and cancer.
XX	
SQ	Sequence 258 BP; 55 A; 82 C; 65 G; 55 T; 1 other;
XX	
Query Match	7.1%; Score 222.2; DB 21; Length 258;
Best Local Similarity	92.5%; Pred. No. 6.2e-47;
Matches 233; Conservative	0; Mismatches 19; Indels 0; Gaps 0.
QY	290 cagagtcagtcgtgtggcagacagtccttcataccaccctggcgcacacgctcc 349
Db	1 cagatgtgcagccggtgtggcagacagtccttcataccaccctggcgcacacgctcc 60
QY	350 tcatccaglttgcacaccccaagatttcgttcttcttacaacactcctgaacactgtc 409
Db	61 tcatccaglttgcacaccccaagatttcgttcttcttacaacactcctgaacactgtc 120
QY	410 gggggcacaacctggagagctctgtgttcacgtgacgcgacagaagaatcctacgtctgc 469
Db	121 gggggcacaacctggagagctctgtgttcacgtgacgcgacagaagaatcctacgtctgc 180
QY	470 agtacttcagttcatgtgtctacatccaccagacagacaactgtgtcagagactatgtgc 529
Db	181 agtacttcagttcatgtgtctacatccaccagacagacaactgtgtcagagactatgtgc 240
QY	530 ggacagcgacct 541
Db	241 ggacagcgacct 252
RESULT	9
ID	Z46039 standard; CDNA; 256 BP.
XX	Z46039;
AC	
XX	25-APR-2000 (first entry)
DT	
XX	
DE	Partial CDNA encoding a transferase designated HUYRAN-3 fragment.
XX	
KW	Transferase; HUYRAN-3; arginine methyltransferase; autoimmune disorder;
KW	inflammatory disorder; AIDS; atherosclerosis;
KW	adult respiratory distress syndrome; allergy; asthma; trauma;
KW	autoimmune thyroiditis; bronchitis; Crohn's disease; diabetes mellitus;
KW	gout; Grave's disease; osteoarthritis; osteoporosis; pancreatitis;
KW	psoriasis; rheumatoid arthritis; infection; neurological disorder;
KW	epilepsy; ischemic cerebrovascular disease; stroke; Alzheimer's disease;
KW	picks disease; Huntington's disease; dementia; Parkinson's disease;
KW	extrapyramidal disorder; viral central nervous system disease;
KW	prion disease; central nervous system developmental disorder;
KW	neuroskeletal disorder; muscular dystrophy; neuromuscular disorder;
KW	peripheral nervous system disorder; mental disorder; schizophrenia;
KW	anxiety; reproductive disorder; gastrointestinal disorder; dyspepsia;
KW	indigestion; gastritis; anorexia; nausea; abdominal angina;
KW	gastroenteritis; intestinal obstruction; peptic ulcer;
KW	irritable bowel syndrome; diarrhoea; constipation;
KW	gastrointestinal haemorrhage; cancer; ss.
XX	
OS	Homo sapiens.
XX	
PN	WO200000594-A2.
XX	
PD	06-JAN-2000.
XX	
FE	29-JUN-1999; 99WO-US14651.
XX	
RS	30-JUN-1998; 98US-0109204.

XX (INCY-) INCYTE PHARM INC.
 PA
 PI Lal P, Bandman O, Hillman JL, Guegler KJ, Gorgone GA, Corley NC,
 PI Patterson C;
 XX WPI: 2000-147267/13.
 DR
 XX
 XX Novel human transferases used for the diagnosis, treatment, and
 PT prevention of autoimmune/inflammatory, neurological, reproductive and
 PT gastrointestinal disorders and cancer
 XX
 PS Disclosure: Page 89; 95pp; English.
 XX
 XX 246039-47 represent partial fragments which were used to produce Incyte
 CC clone 2525071, which encodes a transferase polypeptide, designated
 CC HUTRAN-3. The polypeptide is an arginine methyltransferase. The
 CC HUTRAN polypeptides, polynucleotides, agonists, antagonists, and
 CC antibodies can be used to diagnose, treat or prevent autoimmune/
 CC inflammatory diseases (e.g. AIDS, adult respiratory distress syndrome,
 CC Crohn's disease, diabetes mellitus, gout, Grave's disease,
 CC osteoarthritis, osteoporosis, pancreatitis, psoriasis, rheumatoid
 CC arthritis, infections, trauma, neurological disorders (e.g. epilepsy,
 CC ischemic cerebrovascular disease, stroke, Alzheimer's disease, Pick's
 CC disease, Huntington's disease, dementia, Parkinson's disease and other
 CC extrapyramidal disorders), viral central nervous system disease, prion
 CC diseases, central nervous system developmental disorders, neuroskeletal
 CC disorders, muscular dystrophy, neuromuscular disorders, peripheral
 CC nervous system disorders, mental disorders, schizophrenic, anxiety,
 CC reproductive disorders and gastrointestinal disorders (e.g. dyspepsia,
 CC indigestion, gastritis, anorexia, nausea, abdominal angina,
 CC gastroenteritis, intestinal obstruction, intestinal tract infections,
 CC peptic ulcer, irritable bowel syndrome, diarrhoea, constipation,
 CC gastrointestinal haemorrhage, and cancer.
 XX
 XX Sequence 256 BP; 54 A; 77 C; 67 G; 58 T; 0 other;
 SQ

Query Match 7.1%; Score 221.4; DB 21; Length 256;
 Best Local Similarity 91.8%; Pred. No. 9.9e-47;
 Matches 234; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

OY 385 ttctacaacatctgaaacacctgtcggggcacaacacgtgagcgtctgttcaagtsg 444
 |||||||
 DB 2 ttctacaacatctgaaacacctgtcggggcacaacacgtgagcgtctgttcaagtsg 61
 OY 445 cggagagaggaatcctcgtgtgagctactccagttatgagctactatcccgagcg 504
 |||||||
 DB 62 cggagagaggaatcctcgtgtgagctactccagttatgagctactatcccgagcg 121
 OY 505 cagaacatgagtgcagagctatgtgcgagacgacactacacgctgcgtcgtcgaagc 564
 |||||||
 DB 122 cagaacatgagtgcagagctatgtgcgagacgacactacacgctgcgtcgtcgaagc 181
 OY 565 cacaacgagctcaaggaagaatcgttctagatgtgagctgtggtcttggatccgtgca 624
 |||||||
 DB 182 cacaacgagctcaaggaagaatcgttctgagtgtgtgtgtgtgtgtgtgtgtgtgtgt 241
 OY 625 tttttgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 639
 |||||||
 DB 242 tttttgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 256
 |||||||

RESULT 10
 ID A00854 standard; CDNA; 300 BP.
 AC A00854;
 XX
 XX 19-MAY-2000 (first entry)
 DT
 XX Human colon cancer cell line polynucleotide sequence SEQ ID NO:845.
 DE

XX Human; colon cancer; tumour; diagnosis; gene expression product;
 KM probe; detection; cancerous state; metastasis; identification;
 KM breast cancer; oestrogen receptor-positive breast cancer; therapy;
 KM oestrogen receptor-negative breast cancer; lung cancer; ss.
 XX
 OS Homo sapiens.
 XX
 XX W09958675-A2.
 PN
 XX 18-NOV-1999.
 PD
 XX
 XX 13-MAY-1999; 99WO-US10602.
 PF
 XX 14-MAY-1998; 98US-0085426.
 PR
 PR 15-MAY-1998; 98US-0085537.
 PR 15-MAY-1998; 98US-0085696.
 PR 21-OCT-1998; 98US-0105234.
 PR 27-OCT-1998; 98US-0105877.
 XX
 PA (CHIR) CHIRON CORP.
 PA (HYSE-) HYSEQ INC.
 XX
 PI Williams LT, Escobedo J, Innis MA, Garcia PD, Sudduth-Klinger J;
 PI Reinhard C, Glese K, Randazzo F, Kennedy GC, Pot D, Kassam A;
 PI Lamson G, Drmanac R, Crkvenjakov R, Dickson M, Drmanac S, Labat I;
 PI Leshkowitz D, Kita D, Garcia V, Jones LW, Stache-Crain B;
 DR WPI: 2000-126369/11.
 XX
 PT Polynucleotide library used to determine cancerous states of mammalian
 PT cells -
 PS
 PS Claim 1; Page 386; 1097pp; English.
 XX
 CC A00010 to A02716 represent polynucleotides isolated from CDNA libraries
 CC constructed from human colon cancer cell lines. The present invention
 CC also describes a method of detecting differentially expressed genes
 CC correlated with a cancerous state of a mammalian cell, comprising
 CC detecting at least one differentially expressed gene product in a test
 CC sample derived from a cell suspected of being cancerous, where detection
 CC of the differentially expressed gene product is correlated with a
 CC cancerous state of the cell from which the test sample was derived.
 CC The polynucleotide sequences can be used in a method for detecting
 CC differentially expressed genes correlated with a cancerous state of a
 CC mammalian cell. The polynucleotides can also be used as probes for
 CC detecting and mapping related genes. They can be used in diagnosis and
 CC prognosis of diseases and disorders (e.g. identification of
 CC pre-metastatic or metastatic cancerous states, stages of cancer, or
 CC responsiveness of cancer to therapy). This is particularly for breast
 CC cancer, oestrogen receptor-positive breast cancer, oestrogen receptor-
 CC negative breast cancer, lung cancer, and colon cancer.
 XX
 XX Sequence 300 BP; 67 A; 101 C; 74 G; 58 T; 0 other;
 SQ

Query Match 6.5%; Score 203.6; DB 21; Length 300;
 Best Local Similarity 85.6%; Pred. No. 3.5e-42;
 Matches 238; Conservative 0; Mismatches 39; Indels 1; Gaps 1;

OY 1375 atcagatgtgtgacagagtgagacagagctccacagctccaaagctcgtgactga 1434
 |||||||
 DB 17 atcagatgtgtgacagagtgagacagagctccacagctccaaagctcgtgactgtg 76
 OY 1435 aagaacccctcttcaggtatcacaggtacacacccatcacccacacgtgtcacactac 1494
 |||||||
 DB 77 aaaaacccctcttcaggtatcacaggtacacacccatcacccacacgtgtcacactac 136
 OY 1495 agcttcctcctcgagagatgtggaacacaggaagcaactataatcgcagcaggggtg 1554
 |||||||
 DB 137 acatctccctcgagagagatgtggaacacaggaagcaactataatcgcagcaggggtg 196
 |||||||
 OY 1555 gctgtgtgtgagatgctactgtcctagacactgtgacaggtgttatgtgcggcggtccagt 1614
 |||||||

CC human protel

RESULT	12
ID	246046
XX	246046 standard; cDNA; 529 BP

246046;
25-APR-2000 (first entry)
Partial cDNA encoding a transferase designated HUTRAN-3 fragment.
Transferase; HUTRAN-3; arginine methyltransferase; autoimmune disorder;
inflammatory disorder; AIDS; atherosclerosis;
adult respiratory distress syndrome; allergy; asthma; trauma;
autoimmune thyroiditis; bronchitis; Crohn's disease; diabetes mellitus;
gout; Grave's disease; osteoarthritis; osteoporosis; pancreatitis;
psoriasis; rheumatoid arthritis; infection; neurological disorder;
epilepsy; ischemic cerebrovascular disease; stroke; Alzheimer's disease;
Pick's disease; Huntington's disease; dementia; Parkinson's disease;
extrapyramidal disorder; viral central nervous system disease;
pilon disease; central nervous system developmental disorder;
neurosis; central nervous system developmental disorder;
peripheral nervous system disorder; mental disorder; schizophrenia;
anxiety; reproductive disorder; gastrointestinal disorder; dyspepsia;
indigestion; gastritis; anorexia; nausea; abdominal angina;
gastroenteritis; intestinal obstruction; peptic ulcer;
irritable bowel syndrome; diarrhoea; constipation;
gastrointestinal haemorrhage; cancer; ss.
Homo sapiens.
WO200000594-A2.
06-JAN-2000.
29-JUN-1999; 99WO-US14651.
30-JUN-1998; 98US-0109204.
(INCYTE) INCYTE PHARM INC.
Lal P, Bandman O, Hillman JL, Guegler KJ, Gorgone GA, Corley NC;
Patterson C;
WPI: 2000-147267/13.
Novel human transferases used for the diagnosis, treatment, and
prevention of autoimmune/inflammatory, neurological, reproductive and
gastrointestinal disorders and cancer
Disclosure: Page 92; 95pp; English.
Z46039-47 represent partial fragments which were used to produce Incyte
clone 2525071, which encodes a transferase polypeptide, designated
HUTRAN-3. The polypeptide is an arginine methyltransferase. The
HUTRAN polypeptides, polynucleotides, agonists, antagonists, and
antibodies can be used to diagnose, treat or prevent autoimmune/
inflammatory diseases (e.g. AIDS, adult respiratory distress syndrome,
allergies, asthma, atherosclerosis, autoimmune thyroiditis, bronchitis,
Crohn's disease, diabetes mellitus, gout, Grave's disease,
osteoarthritis, osteoporosis, pancreatitis, psoriasis, rheumatoid
arthritis, infections, trauma, neurological disorders (e.g. epilepsy,
ischemic cerebrovascular disease, stroke, Alzheimer's disease, Pick's
disease, Huntington's disease, dementia, Parkinson's disease and other
extrapyramidal disorders), viral central nervous system disease, pilon
disease, central nervous system developmental disorders, neuroskeletal
disorders, muscular dystrophy, neuromuscular disorders, peripheral
nervous system disorders, mental disorders, schizophrenia, anxiety,
reproductive disorders and gastrointestinal disorders (e.g. dyspepsia,
indigestion, gastritis, anorexia, nausea, abdominal angina,
gastroenteritis, intestinal obstruction, intestinal tract infections,
peptic ulcer, irritable bowel syndrome, diarrhoea, constipation,
gastrointestinal haemorrhage, and cancer.

Query Match 4.58; Score 139.8; DB 21; Length 529;

Best Local Similarity	77.0%;	Pred. No. 6,9e-26;
Matches	218;	Conservative 0; Mismatches 55; Indels 10; Gaps 4

QY	2295	gcgcagcctctccctaaacacacagggccacatggttacacatggtggtgtttgacgtcgtctt	2355
Db	34	gcgggggccccctccctcgacgacagagctctc--ggtacacagggagcgtgacagctgcgtctt	91
QY	2355	tttaaatcttattttttttaaagaaagaacacagtggtacacccacagacccctctgaagaaac	2414
Db	92	tttaaatatttttttttttaagaaagaacacagtggtacacccagacccctctgtgaagcc	151
QY	2415	cggctcgtg-cggcgccaagccagcgacccctgttcctctatgcccagagag-ttctatggtgaagg	2472
Db	152	agcgccggcgccggcgccgagccagcagccccctctccctaatgactacagagcgccggggaggg	211
QY	2473	gtggcgccgttcaagcctctcagagtggtggacaagccctccacccaagaagggtttcaacctcaa	2533
Db	212	gtmcccgccggaggtctcaagg-----nnmccctccacacaagaagggtttcaactcaaa	265
QY	2533	cttgaatgtatacaaacacacccagctgtcccaagagcctatgcct	2575
Db	266	cttgaatgtatacannccacccactgtgtggagagcctcgcgtctt	308

RESULT	13
Q61313	
ID	Q61313 standard; DNA; 217 BP.

AC Q61313;

DT 16-MAR-1994 (first entry)

DE Human brain Expressed Sequence Tag EST01321

KW Gene transcription product; genetic markers; tagging; in vivo; transcription; mapping; locations; chromosomes; chromosomal; ss

OS Homo sapiens

PN W09316178-A.

PD 19-AUG-1993

PF 12-FEB-1993; 93WO-US01321.

PR 12-FEB-1992; . 92US-0837195.

PA (USSH) US DEPT HEALTH & HUMAN SERVICE.

PI Adams MD, Moreno RF, Venter CJ;

DR WPI: 1993-272882/34.

PT Enriched oligonucleotides and corresp. sequences - used as

PT of most human genes

PS Example 4; Page 471; 500pp; English.

CC The Expressed Sequence Tag was isolated from a human brain cDNA

CC for human genes transcribed in vivo. They can be used to facilitate

CC on chromosomes, for individual or forensic identification, for mapping

CC type, and for prepn. of antisense sequences, probes and constructs.

CC coding-region prediction program CRM. See also Q59041-Q61440.

Sequence 217 BP; 45 A; 76 C; 61 G; 30 T; 5 other,

Query Match	3.98;	Score 123.2;	DB 14;	Length 217;
-------------	-------	--------------	--------	-------------

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: June 20, 2001, 09:55:06 ; Search time 23.09 Seconds
(without alignments)
1505.208 Million cell updates/sec

Title: US-09-464-377-2

Perfect score: 3168
Sequence: 1 MAANAATVGPAGSAGVAG.....PAISNAPSISPTMTMKG 608

Scoring table:
BLOSUM62
Gapop 10.0 , Gapect 0.5

Searched: 390729 seqs, 57163235 residues

Total number of hits satisfying chosen parameters: 390729

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

A.Geneseq 0401:*

1:	/SID6/gcgdata/geneseq/geneseq/AA1980.DAT:*
2:	/SID6/gcgdata/geneseq/geneseq/AA1981.DAT:*
3:	/SID6/gcgdata/geneseq/geneseq/AA1982.DAT:*
4:	/SID6/gcgdata/geneseq/geneseq/AA1983.DAT:*
5:	/SID6/gcgdata/geneseq/geneseq/AA1984.DAT:*
6:	/SID6/gcgdata/geneseq/geneseq/AA1985.DAT:*
7:	/SID6/gcgdata/geneseq/geneseq/AA1986.DAT:*
8:	/SID6/gcgdata/geneseq/geneseq/AA1987.DAT:*
9:	/SID6/gcgdata/geneseq/geneseq/AA1988.DAT:*
10:	/SID6/gcgdata/geneseq/geneseq/AA1989.DAT:*
11:	/SID6/gcgdata/geneseq/geneseq/AA1990.DAT:*
12:	/SID6/gcgdata/geneseq/geneseq/AA1991.DAT:*
13:	/SID6/gcgdata/geneseq/geneseq/AA1992.DAT:*
14:	/SID6/gcgdata/geneseq/geneseq/AA1993.DAT:*
15:	/SID6/gcgdata/geneseq/geneseq/AA1994.DAT:*
16:	/SID6/gcgdata/geneseq/geneseq/AA1995.DAT:*
17:	/SID6/gcgdata/geneseq/geneseq/AA1996.DAT:*
18:	/SID6/gcgdata/geneseq/geneseq/AA1997.DAT:*
19:	/SID6/gcgdata/geneseq/geneseq/AA1998.DAT:*
20:	/SID6/gcgdata/geneseq/geneseq/AA1999.DAT:*
21:	/SID6/gcgdata/geneseq/geneseq/AA2000.DAT:*
22:	/SID6/gcgdata/geneseq/geneseq/AA2001.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2826.5	89.2	551	21	B43316 Human ORFX ORF3080
2	2290.5	72.3	447	21	Y54593 Human acid sequence
3	498.5	15.7	390	21	G24704 Arabidopsis thalia
4	498	15.7	341	21	G24705 Arabidopsis thalia
5	494.5	15.6	353	19	W64203 Arginine methyltra
6	488.5	15.4	357	21	B43525 Human cancer assoc
7	488.5	15.4	361	19	W64202 Human interferon r
8	474.5	15.0	531	21	Y84432 Arabidopsis thalia
9	472.5	14.9	306	21	G24706 Arabidopsis thalia
10	467.5	14.8	339	21	G29547 Arabidopsis thalia
11	467.5	14.8	366	21	G29546 Arabidopsis thalia

12	443.5	14.0	306	21	G29548
13	378	11.9	360	19	W64204
14	299.5	9.5	297	20	Y48597
15	267	8.4	122	20	Y26923
16	183	5.8	97	21	G01996
17	182.5	5.8	193	21	B42019
18	177	5.6	692	21	B49313
19	169.5	5.4	589	19	W54096
20	165	5.2	542	21	G21384
21	165	5.2	599	21	G21383
22	165	5.2	645	21	G21382
23	127.5	4.0	276	19	W30525
24	117	3.7	531	19	W56311
25	114	3.6	1275	20	Y29084
26	114	3.6	1275	21	Y44262
27	108	3.4	356	14	R37715
28	107.5	3.4	1289	13	R20067
29	107.5	3.4	1289	13	R28890
30	107.5	3.4	1289	13	R29027
31	107.5	3.4	1289	13	R28810
32	107.5	3.4	1289	13	R29517
33	107.5	3.4	1289	14	R44202
34	107.5	3.4	1289	15	R58632
35	107.5	3.4	1289	16	R76113
36	107.5	3.4	1289	18	W13885
37	107.5	3.4	1289	21	B13892
38	99	3.1	552	12	R13879
39	98.5	3.1	1071	21	Y97317
40	98.5	3.1	3782	21	Y77179
41	98	3.1	235	19	W98690
42	98	3.1	777	20	Y43091
43	97.5	3.1	331	21	G04327
44	97.5	3.1	331	21	G04327
45	97.5	3.1	985	18	W15191

ALIGNMENTS

RESULT	1
ID	B43316
BA3316	standard; Protein; 551 AA.
AC	B43316;
DT	08-FEB-2001 (first entry)
XX	
DE	Human ORFX ORF3080 polypeptide sequence SEQ ID NO:6160.
KW	Human; open reading frame; ORFX; detection; cytosolic; hepatotropic;
KW	vulnerable; antiposrotic; antiparkinsonian; neotrophic; neuroprotective;
KW	anticonvulsant; osteoprotic; antirheumatic; immunosuppressant; cardiant;
KW	immunostimulant; thrombolytic; coagulant; vasotropic; antidiabetic;
KW	hypotensive; dermatological; immunosuppressive; antineoplastic;
KW	antiviral; antibacterial; antifungal; antineumatic; antihypert;
KW	antianaemic; gene therapy; cancer; proliferative disorder; hypertension;
KW	neurodegenerative disorder; osteoarthritis; graft vs host disease;
KW	cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS;
KW	cholesterol ester storage; systemic lupus erythematosus; infection;
KW	severe combined immunodeficiency; malaria; autoimmune disorder; asthma;
KW	allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound;
KW	bone damage; cartilage damage; antiinflammatory disease; coagulation;
KW	thrombosis; contraceptive.
XX	
OS	Homo sapiens.
XX	
PN	W0200058473-A2.
XX	
PD	05-OCT-2000.
XX	
PF	31-MAR-2000; 2000MO-US08621.
XX	
PR	31-MAR-1999; 9905-0127607.

PR 02-APR-1999; 99US-0127636.
PR 05-APR-1999; 99US-0127228.
PR 30-MAR-2000; 2000US-0540763.
XX (CURA-) CURAGEN CORP.
PI Shinkets RA, Leach M;
XX WPI; 2000-602362/57.
DR N-PSDB; C77525.
XX
PT Novel nucleic acids and peptides derived from open reading frame X,
PT useful for treating e.g. cancers, proliferative disorders,
PT neurodegenerative disorders and cardiovascular disease -
PS
PS
PS Claim 11; Page 5346-5348; 5507pp; English.
XX
CC C74446 to C77606 encode the proteins given in B40237 to B43397, which
CC represent the human ORF open reading frames 1 to 3161. The ORF
CC sequences have activities such as: cytostatic; hepatotropic; vulnary;
CC antiproliferative; antiparinsonian; nootropic; neuroprotective; osteopathic;
CC anticovulsant; antiallergic; immunosuppressant; immunostimulant;
CC cardiact; thrombolytic; coagulant; vasotropic; antidiabetic; hypotensive;
CC dermatological; immunosuppressive; antineoplastic; antibacterial;
CC antiviral; antifungal; antihemorrhagic; antithyroid; and antineoplastic.
CC The sequences can be used for determining the presence of or predisposition
CC to, or preventing or treating pathological conditions associated with an
CC ORF-associated disorder. The nucleic acids can be used to express ORF
CC proteins in gene therapy vectors. The proteins and nucleic acids may be
CC used to treat cancers, proliferative disorders, neurodegenerative
CC disorders, osteoarthritis, graft vs host disease, cardiovascular disease,
CC diabetes mellitus, hypertension, hypothyroidism, cholesterol ester
CC storage, systemic lupus erythematosus, severe combined immunodeficiency
CC (SCID), AIDS, viral, bacterial or fungal infection, malaria, autoimmune
CC disorders, asthma, allergies, aplastic anaemia, burns, wounds, bone and
CC cartilage damage, nocturnal haemoglobinuria, antineoplastic disease; to
CC enhance coagulation; to inhibit thrombosis; and as a contraceptive.
XX
XX Sequence 551 AA:
SQ

Query Match 89.2%; Score 2826.5; DB 21; Length 551;
Best Local Similarity 98.4%; Pred. No. 2.7e-234;
Matches 542; Conservative 6; Mismatches 2; Indels 1; Gaps 1;

QY 59 LEVRAAGPAAGIALYSHEDVCFKCSVSRETCRSVRGROSFITTCNSVLIQFAPPHDF 118
DB 1 LEVRAAGPAAGIALYSHEDVCFKCSVSRETCRSVRGROSFITTCNSVLIQFAPPHDF 60
QY 119 CSFYNIKTRCHRTLEKRSYFSESTRESSAVOYFOFGYISQOONMODYVRCGYORAIL 178
DB 61 CSFYNIKTRCHRTLEKRSYFSESTRESSAVOYFOFGYISQOONMODYVRCGYORAIL 120
QY 179 QHRTPEKDRIVADVCGSGSIIISFFAQAQARKIYAEASTMAQAHAEVLYKSNLJTRIVY 238
DB 121 QHRTPEKDRIVADVCGSGSIIISFFAQAQARKIYAEASTMAQAHAEVLYKSNLJTRIVY 180
QY 239 IFCVKEEVSLEPQVDIIIEPFGYMLFNERMLESYLHAKKYLKPSGNMPEPTIGDVLHAP 298
DB 181 IFCVKEEVSLEPQVDIIIEPFGYMLFNERMLESYLHAKKYLKPSGNMPEPTIGDVLHAP 240
QY 299 TPEOLYMEQFTANRKYOSFSGVDSALRGAVDEYFQPVVDFTDIRLAKKSYKTYV 358
DB 241 TPEOLYMEQFTANRKYOSFSGVDSALRGAVDEYFQPVVDFTDIRLAKKSYKTYV 300
QY 359 NLEAKEGDLHRIEIPFKPHMLHSGVHGLAFWEDVAFISITVWLSTAPTEPLTHWYO 418
DB 301 NLEAKEGDLHRIEIPFKPHMLHSGVHGLAFWEDVAFISITVWLSTAPTEPLTHWYO 360
QY 419 VRCLEQSPLEFANAGDTLSGTCILLIANKROSYDISIAQVDQTSKSSNLLDKNPFERYT 478
DB 361 VRCLEQSPLEFANAGDTLSGTCILLIANKROSYDISIAQVDQTSKSSNLLDKNPFERYT 420

QY 479 GTTPSPPGSHYTSPEENMMNTGSTYNLSSGVAVAGMPTAYDLDSVIAGSSVGHNNLIP 538
DB 421 GTTPSPPGSHYTSPEENMMNTGSTYNLSSGVAVAGMPTAYDLDSVIAGSSVGHNNLIP 480
QY 539 LANTGIVNHTSRMGSIMSTGIVQSSGAQG-GGGSSSAHYAVNNOFTMGAPISMASPM 597
DB 481 LANTGIVNHTSRMGSIMSTGIVQSSGAQG-GGGSSSAHYAVNNOFTMGAPISMASPM 540
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DB 541 SIPTNTMAYGS 551
RESULT 2
Y54593
ID Y54593 standard; Protein; 447 AA.
XX
XX Y54593;
AC XX
DT 25-APR-2000 (first entry)
XX
XX Amino acid sequence of a human transferrase designated HUFAN-3.
DE
XX Transferrase; HUFAN-3; arginine methyltransferase; autoimmune disorder;
XX inflammatory disorder; AIDS; atherosclerosis;
KW adult respiratory distress syndrome; allergy; asthma; trauma;
KW autoimmune thyroiditis; bronchitis; Crohn's disease; diabetes mellitus;
KW gout; Grave's disease; osteoarthritis; osteoporosis; pancreatitis;
KW psoriasis; rheumatoid arthritis; infection; neurological disorder;
KW epilepsy; ischemic cerebrovascular disease; stroke; Alzheimer's disease;
KW Picks disease; Huntington's disease; dementia; Parkinson's disease;
KW extrapyramidal disorder; viral central nervous system disease;
KW prion disease; central nervous system developmental disorder;
KW neuroleptic disorder; muscular dystrophy; neuromuscular disorder;
KW peripheral nervous system disorder; mental disorder; schizophrenia;
KW anxiety; reproductive disorder; gastrointestinal disorder; dyspepsia;
KW indigestion; gastritis; anorexia; nausea; abdominal angina;
KW gastroenteritis; intestinal obstruction; peptic ulcer;
KW irritable bowel syndrome; diarrhoea; constipation;
KW gastrointestinal haemorrhage; cancer.
XX
XX Homo sapiens.
OS
FH Key Location/Qualifiers
FT 1..46
FT Peptide
FT Modified-site
FT 18
FT Modified-site
FT 27..35
FT Region
FT 49..53
FT Modified-site
FT 69
FT Modified-site
FT 71
FT Modified-site
FT 85
FT Modified-site
FT 88..95
FT Region
FT 117..126
FT Region
FT 127
FT Modified-site
FT 165..169
FT Region
FT 191
FT Modified-site
FT 286
FT Modified-site
FT 293
FT Misc-difference
FT Modified-site
FT 330

FT Modified-site /note= "potential phosphorylation site"
 FT 343
 FT Modified-site /note= "potential glycosylation site"
 FT 355
 FT Modified-site /note= "potential phosphorylation site"
 FT 384
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 PN WC200000594-A2.
 XX 06-JAN-2000.
 PD 29-JUN-1999; 99WO-US14651.
 PF 30-JUN-1998; 98US-0109204.
 PR (INCY-) INCYTE PHARM INC.
 PA Lal P, Bandman O, Hillman JL, Guegler KU, Gorgone GA, Corley NC,
 PI Patterson C;
 PI WPI: 2000-147267/13.
 DR N-PSDB; 246024.
 DR Novel human transferases used for the diagnosis, treatment, and
 PT prevention of autoimmune/inflammatory, neurological, reproductive and
 PT gastrointestinal disorders and cancer
 XX Claim 1; Page 79-80; 95pp; English.
 PS The present sequence represents a transferase polypeptide, designated
 XX HTRAN-3. The HTRAN cDNA sequence is derived from Incyte clone
 CC 255071. The sequence is obtained from the partial sequences 246039-47.
 CC The polypeptide is a arginine methyltransferase. The HTRAN polypeptides,
 CC polynucleotides, agonists, antagonists, and antibodies can be used to
 CC diagnose, treat or prevent autoimmune/inflammatory diseases (e.g. AIDS,
 CC adult respiratory distress syndrome, allergies, asthma, atherosclerosis,
 CC autoimmune thyroiditis, bronchitis, Crohn's disease, diabetes mellitus,
 CC gout, Grave's disease, osteoarthritis, osteoporosis, pancreatitis,
 CC psoriasis, rheumatoid arthritis, infections, trauma, neurological
 CC disorders (e.g. epilepsy, ischemic cerebrovascular disease, stroke,
 CC Alzheimer's disease, Pick's disease, Huntington's disease, dementia,
 CC Parkinson's disease and other extrapyramidal disorders), viral central
 CC nervous system disease, prion diseases, central nervous system
 CC developmental disorders, neuroskeletal disorders, muscular dystrophy,
 CC neuromuscular disorders, peripheral nervous system disorders, mental
 CC disorders, schizophrenia, anxiety, reproductive disorders and
 CC gastrointestinal disorders (e.g. dyspepsia, indigestion, gastritis,
 CC anorexia, nausea, abdominal angina, gastroenteritis, intestinal
 CC obstruction, intestinal tract infections, peptic ulcer, irritable bowel
 CC syndrome, diarrhoea, constipation, gastrointestinal haemorrhage, and
 CC cancer.
 XX
 XX Sequence 447 AA;
 SQ

Query Match 72.3%; Score 2290.5; DB 21; Length 447;
 Best Local Similarity 96.7%; Pred. No. 2.2e-186;
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QY 163 MMDYVTRGTGQRAIILQHTDFKDKIVLDVGGSGIISFPAAGARKIYAEASTMOH 222
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 QY 223 AEVLKSNLDRIVIVIGKVEVSLPQVDIIIEPMGYMFMENRMTESYLHAKKYLKP 282
 Db 61 aeavlksnldrlivivlgkveevslpeqvdiisepmgymfmenrmesylhakkylkp 120
 QY 283 SGNNFPTIGDVHLAPFTDEQLMEQFTANRKYOPSEFGVDLSALRGAAVDYEFKQPVVD 342
 Db 121 sgnnfptigdvhlapftdeqlymeqftanrkyopsfngvdlsalrgaavdeyefkpvvd 180
 QY 343 TFDRIILMAKSVKTVNLEAKEGDILHRIEIPKFNHLSGLVHGLAFMFDVAFGSINT 402

Db 181 tfdriilmaksvktyvnleakegdilhrleipkfnhlshglvghlafmfdvafgsgint 240
 QY 403 VMLSTAPTEPLTFHWVQVRLCFOSPLFAKAGDPTSGCCLILANRQSDISIVQVDTGS 462
 Db 241 vmlstaptepltfhwvqvrclfospflakagdpstgscclilankrqsdisivagvdtgs 300
 QY 463 KSNLIDLKNPFRYTGTPSPPGSHYTPSENMMNTGSTYMLSSGVAAGMPTAYDLS 522
 Db 301 ksnlidlknprfrytgtpspgshytpsenmmntgstynlssgmavagmptaydls 360
 QY 523 SVIAGSSVGHNNLPLANTGIVNHTSRMGSTMGTCIVOGSSGAGC-GGSSSAHYAVN 581
 Db 361 sviasgssvghnnlplantgivnhtsrmgstmgtcivogssgagsggssstahyavn 420
 QY 582 NQFTMGPAISMASPMKSIPTNTHYGS 608
 Db 421 sqftmgpaimaspmksiptnthys 447

RESULT 3
 G24704
 ID G24704 standard; Protein: 390 AA.
 XX
 AC G24704;
 XX
 DT 17-OCT-2000 (first entry)
 XX
 DE Arabidopsis thaliana protein fragment SEQ ID NO: 28481.
 XX
 KW Protein identification; signal transduction pathway; metabolic pathway;
 KW hybridisation assay; genetic mapping; gene expression control; promoter;
 KW termination sequence.
 XX
 OS Arabidopsis thaliana.
 PN EP1033405-A2.
 XX
 PD 06-SEP-2000.
 XX
 PF 25-FEB-2000; 2000EP-0301439.
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PR	22-JUL-1999	9905-0145085


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RESULT 7
W64202 ID W64202 standard; Protein: 361 AA.
XX AC W64202;
XX DT 09-NOV-1998 (first entry)
XX DE Human interferon receptor 1 binding protein IRLB4.
XX KW Interferon receptor 1 binding protein; IRLB4; human; tumour;
XX KM cancer; gene therapy; tissue graft; graft survival;
XX KM arginine methyltransferase.
XX OS Homo sapiens.
XX PN W09831796-A1.
XX PD 23-JUL-1998.
XX PF 15-JAN-1998; 98WO-US00671.
XX PR 15-JAN-1997; 97US-0035636.
XX PA (MCIN/) MCINNIS P A.
XX PA (YEDA) YEDA RES & DEV CO LTD.
XX PI Abramovitch C, Chebath JE, Revel M;
XX DR WPI: 1998-414096/35.
XX DR N-PSDB: V44275.
XX PT New isolated interferon receptor binding proteins - used to develop
XX PT products for modulating sensitivity to interferon, e.g. in the
XX PT treatment of tumours or for prolonging graft survival
XX PS Claim 1; Page 39-40; 64pp; English.
XX CC This is a novel human protein, designated interferon receptor
XX CC binding protein 4 (IRLB4), which interacts with the intracytoplasmic
XX CC (IC) domain of the IFNAR1 chain of the interferon type 1 (IFN-alpha,
XX CC beta or omega) receptor. IRLB4 has sequence homology to enzymes
XX CC which utilise S-adenosyl methionine for methylating arginine
XX CC residues in proteins, such as the arginine methyltransferase PRMT1
XX CC (see W64203). It was identified in a two-hybrid screening for
XX CC proteins interacting with the IFNAR1-IC domain; another protein,
XX CC IRLB1 (see W64199), was similarly identified. A cDNA clone (see
XX CC V44275) encoding IRLB4, host cells and expression vectors are
XX CC claimed. DNA encoding IRLB1 and IRLB4 can be used in cancer
XX CC therapy where the increased cellular response to IFN would result
XX CC in a decrease in malignant cell growth and an enhanced response to
XX CC exogenous IFN therapy. Antisense IRLB1 or IRLB4 nucleic acids can
XX CC be used for prolonging tissue or organ graft survival in patients
XX CC as the rejection of these grafts in the host is mediated by the
XX CC histocompatibility antigens (MHC class I) whose synthesis depends
XX CC on the IFN stimulus. The products can also be used in detection
XX CC and diagnosis.
XX SQ Sequence 361 AA;

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Query Match 15.4%; Score 488.5; DB 19; Length 361;
 Best Local Similarity 32.1%; Pred. No. 1e-33;
 Matches 120; Conservative 68; Mismatches 149; Indels 37; Gaps 8;

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QY 157 LSGQGMMDQYVTCGYQRAIILQNHDFKDKIVDVGCGGILSFFAQAQGARIVVEA 216
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Db 50 fgiheemlkdevrtlytynsmfhnrlfkdkvvlidvsgsgtllcmfakagarkvislec 109
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QY 388 LAFWEDVAFIGSTWYTLSTAPTEPLTHWYQVRCLOSPLEFAKGDPLSGCLLIANKRO 447
  :|:| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 274 lvaqfnleferchkrbtgfspspyhkwqtvfyfmedylytkgeelfglgmtrpnkn 333
QY 448 SYDISIVAOVDQNG 461
Db 334 nrddftldldfkq 347

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RESULT 8
 Y84432 ID Y84432 standard; Protein: 531 AA.
 AC Y84432;
 XX DT 25-JUL-2000 (first entry)
 XX DE Amino acid sequence of a human RNA-associated protein.
 XX KM Human: RNA-associated protein; cell proliferation; cancer; inflammation;
 XX KM immune response; reproductive disorder; actinic keratosis;
 XX KM atherosclerosis; arteriosclerosis; bursitis; cirrhosis; hepatitis;
 XX KM mixed connective tissue disease; myelofibrosis; primary thrombocythemia;
 XX KM paroxysmal nocturnal hemoglobinuria; polycythemia vera; psoriasis;
 XX KM trauma.
 XX OS Homo sapiens.
 XX FH Key Location/Qualifiers
 FT Modified-site 27 /note- "potential phosphorylation site"
 FT Modified-site 58 /note- "potential phosphorylation site"
 FT Modified-site 59 /note- "potential phosphorylation site"
 FT Modified-site 89 /note- "potential phosphorylation site"
 FT Modified-site 155 /note- "potential phosphorylation site"
 FT Modified-site 157 /note- "potential glycosylation site"
 FT Modified-site 242 /note- "potential phosphorylation site"
 FT Modified-site 339 /note- "potential phosphorylation site"
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 FT Modified-site /note- "potential glycosylation site"

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Db 1 mlkdvrtktygnvlygnkflkdklvldvgagtgllstfcakagaaivvyavecsqmdm 60
QY 223 AEVYKSNLTDRIYVPGKVEEVSIP-EOYDIITSEPMGYMLFNERMLESYLHAK-KYL 280
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QY 281 KPSGNMFTIGDVHIAFTEQOLYMEQFTKANFRYQPSFHGVDLSALGAAVDEYFRQPV 340
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PR 29-OCT-1999; 99US-0162142.

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Best Local Similarity 35.98; Pred. No. 6e-32;

Matches 112; Conservative 54; Mismatches 133; Indels 13; Gaps 6;

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QY 205 QAGARKIYAVEASTMAGHAELVKSNNLTDRIVVPGKVEEVSLE-EOVDIIISPEKIM 263
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Db 76 kagaahyavecsqmadtakeivksngfsdvlylkyteetelpvphvdvllsewmyf 135
QY 264 LFNERNLESTYLHAK-KYLKPSGNNEPRTIGDVHLAPFTDEOLYMEQFTANRYPQSPFGV 322
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Db 136 llyenmldvlyanrkwdqglvpdkaslyvalaed-----ahykdkdvefwddvylf 190
QY 323 DLSALRGAAVDEYRQFVDFD-IRILMAKSVKVTWNFLFAKEDGLHRIEIPKFNHIL 381
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QY 382 SGLVHGIAFMDVAFTGISIMTWLSTAPTEPLTHMYOVRCLFQSFLEKAKDGLSGTCLL 441
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QY 442 IANKROSYDISI 453
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Db 306 agnknpdvdl 317

RESULT 11
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ID G29546 standard. Protein; 366 AA.
XX
AC G29546;
XX
DT 17-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana protein fragment SEQ ID NO: 35174.
XX
KW Protein identification; signal transduction pathway; metabolic pathway;
KM hybridisation assay; genetic mapping; gene expression control; promoter;
KM termination sequence.
XX
OS Arabidopsis thaliana.
XX
PN EP1033405-A2.
XX
PD 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-0301439.
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DT 17-OCT-2000 (first entry)
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KM Protein identification; signal transduction pathway; metabolic pathway;
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KM termination sequence.
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Query Match	14.0%;	Score 443.5;	DB 21;	Length 306;
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Matches 107;	Conservative 51;	Mismatches 123;	Indels 13;	Gaps 6

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OY 163 MM0DYPRG1GT0RAL1N0NDHDFKRY1VL0VCGSGG1LSFPA0AGAK1TAVEASTYAOH 222
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OY 261 KP5GNMFTJGDVHLAPRTDQULYMEQFTKANFYOP5HGVDLSALRGAAVDYEROPV 340
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KM	HCP-1; IR134; Interferon receptor 1 binding protein 4; human
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PN	W09831796-A1.
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PI	Abramovitch C, Chebath JE, Revel M;
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DR	WPI:1998-414096/35.

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: June 20, 2001, 09:55:06 ; Search time 22.66 Seconds

(without alignments)
2043.871 Million cell updates/sec

Title: US-09-464-377-2

Sequence: 1 MAAATAATGAGGAGSAGVAG.....PAISMASPSIPTMTMHGYS 608

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :
1: p1r1:***
2: p1r2:***
3: p1r3:***
4: p1r4:***

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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1	498.5	15.7	390	2 T09914	protein-arginine N
2	496.5	15.7	376	2 T52248	protein-arginine N
3	486	15.3	348	2 S45890	ODP1 protein - Yea
4	477.5	15.1	383	2 A86182	hypothetical prote
5	472.5	14.9	339	2 T50263	probable arginine
6	467.5	14.8	366	2 F84579	hypothetical prote
7	449.5	14.2	428	2 T26447	hypothetical n-methyl
8	374	11.8	472	2 T40755	related to protein
9	349	11.0	521	2 T49355	hypothetical prote
10	172	5.4	630	2 T26236	flission yeast Skbl
11	170.5	5.4	637	2 T03842	hypothetical prote
12	163	5.1	670	2 T10666	conserved hypotet
13	146	4.6	259	2 C64481	hypothetical prote
14	138	4.4	680	2 T25146	hypothetical prote
15	123.5	3.9	271	2 T41026	probable methyltra
16	122.5	3.9	638	2 F75025	cytochrome 2 - hu
17	120.5	3.8	208	2 F75025	methyltransferase
18	120.5	3.8	1077	2 S45395	hypothetical prote
19	119.5	3.8	827	2 S46002	probable membrane
20	118	3.7	245	2 D82221	3-demethylubiquino
21	115	3.6	296	1 T64105	ribosomal protein
22	114	3.6	387	2 A81324	cyclopropane-fatty
23	114	3.6	819	2 T08745	probable RNA helic
24	112.5	3.6	207	2 D71210	hypothetical prote
25	112.5	3.6	267	2 A72238	hemolysin - Thermo
26	112.5	3.6	529	2 T23431	hypothetical prote
27	112.5	3.6	1997	2 T30874	virginiamycin S sy
28	111	3.5	258	2 H70367	hemolysin - Aquife
29	111	3.5	1032	2 T34433	hypothetical prote

30	111	3.5	1755	2 S69951	TyB protein - yea
31	111	3.5	2232	2 T34434	hypothetical prote
32	110	3.5	197	2 H64415	hypothetical prote
33	109.5	3.5	311	1 C69952	probable ribosomal
34	109	3.4	1755	2 S69866	TyB protein - yea
35	108	3.4	356	2 A47128	carbamimycin 4-O-m
36	107.5	3.4	295	2 D82341	ribosomal protein
37	107.5	3.4	1289	2 T18212	parasporeal crystal
38	107	3.4	690	2 T33109	hypothetical prote
39	106.5	3.4	245	2 J04185	proteinase II (EC
40	106.5	3.4	245	2 B86738	hypothetical prote
41	106.5	3.4	967	2 S66852	hypothetical prote
42	106	3.3	216	2 A72345	conserved hypotet
43	106	3.3	316	2 T43740	probable ribosomal
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45	105	3.3	251	2 B64048	hypothetical prote

ALIGNMENTS

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protein-arginine N-methyltransferase (EC 2.1.1.23) - Arabidopsis thaliana
N:Alternate names: protein T16L4.20
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 05-May-2000
C:Accession: T09914
R:Bayan, M.; Rose, M.; Hempel, S.; Entian, K.D.; Bancroft, I.; Mewes, H.W.; Mayer, K.
submitted to the Protein Sequence Database, June 1999
A:Reference number: Z16897
A:Accession: T09914
A:Molecule type: DNA
A:Residues: 1-390 <BEV>
A:Cross-references: EMBL:AL079344; GSPDB:GN00062; ATSP:T16L4.20
A:Experimental source: cultivar Columbia; BAC clone T16L4
C:Genetics:
A:Gene: pam1; ATSP:T16L4.20
A:Map position: 4
A:introns: 80/1; 83/3; 135/3; 157/1; 204/3; 234/1; 272/3; 323/1
C:Keywords: methyltransferase; S-adenosylmethionine

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QY 174	ORATIQNTDFDKITLVLDVCGSGGILTFPAOAGARKIYAVASTMAOAEVLKSNNT	233			
DB 96	QNVITQNFELIKDKITLVLDVAGAGTILSLFCARAGAAHYAVCSQADNAKELVANKGS	155			
QY 234	DRIVVIPKGVKEVSLP-EQVDIIIESEPMGYLNFERNMLESYLAH-KYLKPSGNMPTIG	291			
DB 156	DVITVLKKGIEIEIETPKVDVILISEMMGYFLFEMLDLSVLYARDKMLVEGVLPDKA	215			
QY 232	DVHLAPFDEQLMEQFLKANKRFRYQPSFGVLSALRGAAVDYFRQPVVDFDIRILMA	351			
DB 216	SLHLTAID-----SEYKEDIETFNWSYGFDMSCIKKAKME---PLVDVDOQNIYT	266			
QY 352	KS-VKVTNPLFAKRGDDHRIEIPKRFHLSGLVHGLAFWDAFVIGSIMVNSTAPT	410			
DB 267	DSRLKTKMDISKSSGDA-SFAFKLVAAQRNDYHALVAIYDVSTFMCHKLLGSTGK	325			
QY 411	EPLTHMYQVRCLEFOSPLFAKAGDTLSGCLLANKROSYDISI	453			
DB 336	SRATHWQTVLYLEVDVLTICBETITGTMSVSPNKKNPDI	368			

RESULT 2

T52248

protein-arginine N-methyltransferase (EC 2.1.1.23) [imported] - Arabidopsis thaliana (fr

C:Species: Arabidopsis thaliana (mouse-ear cross)

C:Date: 20-Oct-2000 #sequence_revision 20-Oct-2000 #text_change 17-Nov-2000

C:Accession: T52248

R:Salchert, K.

submitted to the EMBL Data Library, July 1998

A:Reference number: Z26000

A:Accession: T52248

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-376 <SAL>

A:Cross-references: EMBL:AJ007582; PIDN:CAA07570.1

C:Genetics:

A:Gene: pam1

C:Keywords: methyltransferase; S-adenosylmethionine

Query Match 15.7%; Score 496.5; DB 2: Length 376;

Best Local Similarity 36.4%; Pred. No. 1.7e-29;

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Qy 174 ORAILQNHTEFKDKIVLDVGCSSGILSFPAQAQARKIYAEASTMAQAEVLKSNNTL 233

Db 96 QNVYQNKFLDKDKIVLDVAGAGTGLSLFCAXAGAHYAVECSQADMAKEIVKANGFS 155

Qy 234 DRIVVPGVEVSLP-EQVDIIISFPMGYMLFNERMLESYLHAK-KYLKPSNMPTIG 291

Db 156 DVIYVKGKIEIELEPTFPYVDVLIISWMGYFLLENNMLDSVLYARKMVLGGVLPDKA 215

Qy 232 DVHLAPFDEQLYMEQFTKANFRYQPSFPGVDLSALGCAVDEYFRQPVYDFDIRILMA 351

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Qy 326 SRATHMKQTVLYLEVDLTICEGETITGTMSVSPNKKNPRIIDI 368

Db 326 SRATHMKQTVLYLEVDLTICEGETITGTMSVSPNKKNPRIIDI 368

Qy 326 SRATHMKQTVLYLEVDLTICEGETITGTMSVSPNKKNPRIIDI 368

Db 326 SRATHMKQTVLYLEVDLTICEGETITGTMSVSPNKKNPRIIDI 368

Qy 326 SRATHMKQTVLYLEVDLTICEGETITGTMSVSPNKKNPRIIDI 368

Db 326 SRATHMKQTVLYLEVDLTICEGETITGTMSVSPNKKNPRIIDI 368

A>Note: the nucleotide sequence was submitted to the EMBL Data Library, November 1993

R:Loubardi, A.; Karst, F.; Guilloton, M.

submitted to the EMBL Data Library, December 1993

A:Description: Cloning and sequencing the PDX3 gene encoding pyridoxine (pyridoxamine

A:Reference number: S41301

A:Accession: S41302

A:Molecule type: DNA

A:Residues: 1-55 <LOW>

A:Cross-references: EMBL:X76992

R:Loubardi, A.; Marcitreau, C.; Karst, F.; Guilloton, M.

J. Bacteriol. 177, 1817-1823, 1995

A:Title: Sterol uptake induced by an impairment of pyridoxal phosphate synthesis in S

ase.

A:Reference number: A56147; MDID:95204349

A:Accession: B56147

A:Molecule type: DNA

A:Residues: 1-55 <LOW>

A:Cross-references: GB:X76992

C:Genetics:

A:Gene: SGD:HMT1; ODP1

A:Cross-references: MIPS:YBR034c; SGD:S0000238

A:Map position: 2R

A>Note: YBR034c

C:Superfamily: bioc. homology

C:Keywords: transmembrane protein

F:59-165/Domain: bioc. homology <BIOC>

F:61-77/Domain: transmembrane #status predicted <TM>

Query Match 15.3%; Score 486; DB 2: Length 348;

Best Local Similarity 36.5%; Pred. No. 9.4e-29;

Matches 120; Conservative 56; Mismatches 121; Indels 32; Gaps 9;

Qy 139 SEPTRESSAVQ-YEOPFYGLSQOQNMMDYRTGYQRAILQNHTEFKDKIVLDVCGSG 197

Db 11 TEKTKLSESPQHFNFSNDHYGIHEMLQDTVRLTSYNALIQNKDLFKDKIVLDVCGSG 70

Qy 198 ILSFPAQAQARKIYAEASTMAQAEVLKSNNTLRIYVIGKVEVSLP-EQVDII 256

Db 71 ILSFPAQAQARKIYAEASTMAQAEVLKSNNTLRIYVIGKVEVSLP-EQVDII 130

Qy 257 SEPFGVYLFNERMLESYLHAK-KYLKPSNMPTIGVHLAPFDEQLYMEQFTKANFRY 315

Db 131 SEMMGYFLYLSMMDYLYARKMVLGGVLPDKA-KYLKPSNMPTIGVHLAPFDEQLYMEQFTKANFRY 185

Qy 316 QPSFGVYLSALGCAVDEYFRQPVYDFDIRILMAKSVTYVNFLEAK--EGDLARIET 373

Db 186 QPDYVYGFDSYSPF---VPLVLEPIYDVE-----RNNTVTSQKLIIEFDLNTYKI 232

Qy 374 P-----EFKFNHLSGLVHGLAFWEDVAFIG--SITVWLSTAPTPLTHMYQVRCFLQ 424

Db 233 SDLAFSKSNFKTLAKRQDMGIYTWFDIVPAPKGRKRVESSTGPHAPYTHMKOTIFYFP 292

Qy 425 SPLFAKAGDTLSGCLLIANKROSIDISI 453

Db 293 DDLDAGTGTIEGBLVCSPEKNKRNRLNTI 321

Qy 321 DDLDAGTGTIEGBLVCSPEKNKRNRLNTI 321

Db 321 DDLDAGTGTIEGBLVCSPEKNKRNRLNTI 321

Qy 321 DDLDAGTGTIEGBLVCSPEKNKRNRLNTI 321

Db 321 DDLDAGTGTIEGBLVCSPEKNKRNRLNTI 321

Qy 321 DDLDAGTGTIEGBLVCSPEKNKRNRLNTI 321

Db 321 DDLDAGTGTIEGBLVCSPEKNKRNRLNTI 321

Qy 321 DDLDAGTGTIEGBLVCSPEKNKRNRLNTI 321

Db 321 DDLDAGTGTIEGBLVCSPEKNKRNRLNTI 321

Qy 321 DDLDAGTGTIEGBLVCSPEKNKRNRLNTI 321

Db 321 DDLDAGTGTIEGBLVCSPEKNKRNRLNTI 321

Qy 321 DDLDAGTGTIEGBLVCSPEKNKRNRLNTI 321

Db 321 DDLDAGTGTIEGBLVCSPEKNKRNRLNTI 321

Qy 321 DDLDAGTGTIEGBLVCSPEKNKRNRLNTI 321

Db 321 DDLDAGTGTIEGBLVCSPEKNKRNRLNTI 321

Qy 321 DDLDAGTGTIEGBLVCSPEKNKRNRLNTI 321

Db 321 DDLDAGTGTIEGBLVCSPEKNKRNRLNTI 321

Qy 321 DDLDAGTGTIEGBLVCSPEKNKRNRLNTI 321

Db 321 DDLDAGTGTIEGBLVCSPEKNKRNRLNTI 321

Qy 321 DDLDAGTGTIEGBLVCSPEKNKRNRLNTI 321

Db 321 DDLDAGTGTIEGBLVCSPEKNKRNRLNTI 321

Qy 321 DDLDAGTGTIEGBLVCSPEKNKRNRLNTI 321

Db 321 DDLDAGTGTIEGBLVCSPEKNKRNRLNTI 321

Qy 321 DDLDAGTGTIEGBLVCSPEKNKRNRLNTI 321

Db 321 DDLDAGTGTIEGBLVCSPEKNKRNRLNTI 321

Qy 321 DDLDAGTGTIEGBLVCSPEKNKRNRLNTI 321

Db 321 DDLDAGTGTIEGBLVCSPEKNKRNRLNTI 321

Qy 321 DDLDAGTGTIEGBLVCSPEKNKRNRLNTI 321

Db 321 DDLDAGTGTIEGBLVCSPEKNKRNRLNTI 321

Qy 321 DDLDAGTGTIEGBLVCSPEKNKRNRLNTI 321

Db 321 DDLDAGTGTIEGBLVCSPEKNKRNRLNTI 321

T26447
 hypothetical protein Y113G7B.17 - *Caenorhabditis elegans*
 C:Species: *Caenorhabditis elegans*
 C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
 C:Accession: T26447
 R:Jennard, N.
 submitted to the EMBL Data Library, September 1999
 A:Reference number: Z20215
 A:Accession: T26447
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1348 <MIL>
 A:Cross-references: EMBL:AL110477, NID:e1542121; PIDN:CAB54335.1; CESP:Y113G7B.17
 A:Experimental source: clone Y113G7B
 C:Genetics:
 A:Gene: CESP:Y113G7B.17
 A:Introns: 90/3; 297/3

Query Match 14.2%; Score 449.5; DB 2; Length 348;
 Best Local Similarity 32.9%; Pred. No. 5,1e-26;
 Matches 115; Conservative 62; Mismatches 144; Indels 29; Gaps 8;

QY 125 LKTCRGITLRSVSEETEE-SSAVQYFOFYGYLSQOONMADYVRGTGYRAILQNTHTD 183
 DB 1 MSTENGSADAPVAPAPAKELTSKDYFDSTAHGHEMLKDEVRTTYRNSIYHNSHL 60
 QY 184 FKDKIVADVCGSGILSFFAQAQARKIYAVEASTMAQHAELVKSNNLTDRIVYIPGKY 243
 DB 61 FKDKIVADVCGSGITSLMFAKAKAKKVFAMFESNMALTSKTIADNNLDHIVEYIAKV 120
 QY 244 EYV-SLP---EQVDIIISBPQYMLFNERMLESTYIAH-KYIKPSGNPFPTIGDVHLAPF 298
 DB 121 EDVHELPGIEKVDIIISSEMGYCLFYESMLNTVLAEDRMILAPNGMLFPDKARLYVCAI 180
 QY 299 TDBELVMEQTKANFRQPSFHGVDLSALRGAAVDEYRQGVNPTFDRIIMAKSVKTYV 358
 DB 181 ED-----ROYKEDIHWDSDYGFNMSAIKVAI---KEPLVDIVD-----NAQVNT 224
 QY 359 NPLFAKSGDHLIRI-----PFFHMLHSLVGLAFMFDAVFIGSINTVWLSTAPTE 411
 DB 225 NNCILKAVDLTYVKTIELDFKSDPKLRCRTRSDYIQAFYFTFVESHKCHKTGFSTGPDV 284
 QY 412 PLTHWYVRCIFQSPFLPAKAGDTLSGTCCLIANKRQSTDISIVAQVDQTG 461
 DB 285 QYFHWKQTVFLKDALVTKGSEITGSEMAPNKNNERDLINISFDRKG 334

RESULT 8
 T40755
 arginine n-methyltransferase - fission yeast (*Schizosaccharomyces pombe*)
 C:Species: *Schizosaccharomyces pombe*
 C>Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
 C:Accession: T40755
 R:Lyne, M.; Rajandream, M.A.; Barrell, B.G.; Lauber, J.; Hilbert, H.; Duesterhoeft, A.
 submitted to the EMBL Data Library, March 1998
 A:Reference number: Z21948
 A:Accession: T40755
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1472 <LYN>
 A:Cross-references: EMBL:AL020772; PIDN:CA117825.1; GSPDB:GN00067; SPDB:SPBC8D2.10C
 A:Experimental source: strain 972h-; cosmid c8D2
 C:Genetics:
 A:Gene: SPDB:SPBC8D2.10C
 A:Map position: 2

Query Match 11.8%; Score 374; DB 2; Length 472;
 Best Local Similarity 28.0%; Pred. No. 3,6e-20;
 Matches 133; Conservative 65; Mismatches 169; Indels 108; Gaps 16;

QY 30 VSVFP-GARLLITGDANCEIORHAE-QQALLREVRAGPDAGIALYSHEDVCYFKCSVSR 87

DB 61 ISVLPDDSVLFSLGD---ELDSFEDDNTLELEVENPAD-----VSK 99
 QY 88 ETECSRVRGSEFIITLGCNSVLIOGATPHDFCSFNILKTCRGHTLERSVFSEETEESSA 147
 DB 100 DAELIKKLQ-----NOLI-----SOLEIKDKM-NELTSQTDQLSV 138
 QY 148 V-----QYFOFYGYLSQOONMADYVRGTGYRAILQNTHTDCKRIVLDVCGSGGIL 199
 DB 139 TPKRADNSYFEESYAGNDIHPLMLNDSVRTEGDFYVHNKHIFAGKVLVDVCGGTGL 198
 QY 200 SFFAQAQARKIYAVEASTMAQHAELVKSNNLTDRIVYIPGKYVEEVSIP-EQVDIIISBP 258
 DB 199 SMFCFAKAKKRYAANDSDIIOAMISNAFENGLAQIIFIRKIDISLPLVGKVDIIISE 258
 QY 259 PMGYMLFNERMLESTYIAH-KYIKPSGNPFPTIGDVHLAPFDEOLYMEQF----- 309
 DB 259 WKGVALTFESMIDSVLVARDRFLAPSGIMABSETVLATNTLELPEIDFMSDVYGF 318
 QY 310 KANFRQPSFHGVDLSALRGAAVDEYRQPVV-DTFDIRIIMAKSVKTYVNFLEAKGDL 368
 DB 319 KNGMKDASYGVSVOVPPQTYVN---AKPVYFARFNHMTCKVQDVSEF----- 364
 QY 369 HRIELPFFHMLHSLVGLAFMFDAVFIGSINTVWLSTAPTEPL----- 413
 DB 365 ---SPFLIIDNEGPLAFTLWFDYF-----TYKRQPIPEAIDEACGFTTGQ 411
 QY 414 ---THWYVRCIFQSPFLPAKAGDTLSGTCCLIANKRQSTDISIVAQVDQTGSKSS 465
 DB 412 GTPTHMKQCVLLRRRPLQKCTRYEGTISFSKNNKNNRDDISVHWNVNGADS 466

RESULT 9
 T49355
 related to protein arginine N-methyltransferase 3 [imported] - *Neurospora crassa*
 N:Alternate names: protein Bld1.90
 C:Species: *Neurospora crassa*
 C>Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 02-Jun-2000
 R:Schulte, U.; Aign, V.; Hohelsel, J.; Brandt, P.; Partmann, B.; Holland, R.; Nyakatu
 submitted to the Protein Sequence Database, May 2000
 A:Reference number: Z25022
 A:Accession: T49355
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-521 <SCH>
 A:Cross-references: EMBL:AL355927; GSPDB:GN00116; NCSP:Bld1.90
 A:Experimental source: BAC clone Bld1; strain OR74A
 C:Genetics:
 A:Gene: NCSP:Bld1.90
 A:Map position: 6
 A:Introns: 33/1

Query Match 11.0%; Score 349; DB 2; Length 521;
 Best Local Similarity 29.9%; Pred. No. 3,1e-16;
 Matches 95; Conservative 53; Mismatches 106; Indels 64; Gaps 10;

QY 143 EESSAVQYFOFYGYLSQOONMADYVRGTGYRAILQNTHTDCKRIVLDVCGSGGILSFF 202
 DB 168 KEGASDYFESTAHNDIHETMLKDYVKTATYADFIIQNKDLEFAGKVLVDIGCGTGILSNF 227
 QY 203 AAQAQARKIYAVEASTMAQHAELVKSNNLTDRIVYIPGKYVEEVSIP-EQVDIIISBPNG 261
 DB 228 CAKAGAKQYIAVDRSEIIDKARENITANGLSVITLKRIREVILIPVEKVDIYSEMMG 287
 QY 262 YMLFNERMLESTYIAH-KYIKPSGNPFPTIGDVHLAPFDEOLYMEQFKANFRYQPSH 320
 DB 288 YCLLEAMINSLVLMARDYTLAPQGLVPSHGNNWLP-VSEQELYAEVYD---FWRDYV 342
 QY 321 GVDLSALRGAAVDEYRQPV-----VDFDIRIIMAKSVKTYVNFLEA---KEG 366
 DB 343 GFDKRVQV-KGIYEDCRMEYRPAETVCCGPASFGLLDHFVAVEDLVFTAKMQSAPDQKA 401

QY 367 DLHRIEIPKFMHLSGLVHGLAFWEDYAF-----TGSIMTVML----- 405
 Db 402 ESH-----DGLVWMDVFFARNRVDESIIKIDTKAOWVAETAGKGDKD 445
 QY 406 -----STAPTEPLTHWYQ 418
 Db 446 ARVAFITGPFGEPFTHMQ 463
 RESULT 10
 T26236
 hypothetical protein W06D4.4 - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
 C:Accession: T26236
 R:Kershaw, J.
 submitted to the EMBL Data Library, November 1998
 A:Reference number: 220178
 A:Accession: T26236
 A>Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-630 <WILL>
 A:Cross-references: EMBL:AL034364; NID:e1356156; PIDN:CAA22252.1; GSPDB:GN00019; CESP:W06D4
 A:Experimental source: clone W06D4
 C:Genetics:
 A:Gene: CESP:W06D4.4
 A:Map position: 1
 A:Introns: 30/2; 72/1; 200/1; 296/3; 359/3; 465/3; 553/2
 Query Match 5.4%; Score 172; DB 2; Length 630;
 Best Local Similarity 23.8%; Pred. No. 7.3e-05;
 Matches 63; Conservative 45; Mismatches 99; Indels 58; Gaps 10;
 QY 162 NMADYVRTGYQRAIL-----QNHTEPKDKI-VLDVCGSGSITSFPAQAGARRIYAVE 215
 Db 35 DMILDFRNDKFLAGLTKTIAEKHEMTDGVHYLDIGTGILSLMARECADVTALE 94
 QY 216 A-STMAQHAELVYKSNLTDRIIVYIPGKVEEYSL--PEOVDIIEPFGYMLFNEBMLES 272
 Db 95 VFKMGDCARRITTSNPSMDSKITIYISERTYSQIGSRADITVAEVDTELGALRT 154
 QY 273 YLHA-KRYLKSNGMFPITGIVHLPFTDEOLYMEQFTKAFRYOPSPFG-----VDLSAL 327
 Db 155 FKELERLAKPGCRVYPTGIVYIYPVESHLKM-----FNDIPRLNGEDEEPLGRG 207
 QY 328 RGAADVDFRQPVYDTRDIRILMAKSVYTVNFEAKEGDLHRIIPKFMHLR----- 381
 Db 208 SGTAA-----VDDVQVSEKMTHEFR-----ELSEPIVAKFDFEHEEKIIF 248
 QY 382 -----SGLVHGLAFWFDV 394
 Db 249 DESFVREAVAHSSGTIDALLMMWDI 273
 RESULT 11
 T03842
 fission yeast Skb1 protein homolog - human
 C:Species: Homo sapiens (man)
 C>Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 16-Feb-2001
 C:Accession: T03842
 R:Marcus, S.
 submitted to the EMBL Data Library, July 1997
 A:Description: SKB1HS, a human homolog of the fission yeast skb1 gene.
 A:Reference number: Z15114
 A:Accession: T03842
 A>Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-637 <NAR>
 A:Cross-references: EMBL:AF015913; NID:g2323409; PIDN:AAB66581.1; PID:g2323410
 C:Genetics:
 A:Gene: SKB1HS

C:Superfamily: Schizosaccharomyces pombe negative regulator of mitosis skb1
 Query Match 5.4%; Score 170.5; DB 2; Length 637;
 Best Local Similarity 22.8%; Pred. No. 9.6e-05;
 Matches 94; Conservative 58; Mismatches 152; Indels 109; Gaps 19;
 QY 99 FITTIGCSNVLQIPATPHDPCSPFNILKTCRGHTLERSVSEPTTESSAVQYQFYGLS 158
 Db 264 FIIT-GTN-----HSEKEFCSYLYYLE-----YLSQRPPPNAYELFA-KGYED 306
 QY 159 QOONMMQ-----DYVRTGYQRAIL-----QNHTEPKDKIIVDVCG 194
 Db 307 YLQSPLOPLMDNESQTYVEFEKDPKISQYQDAITKCLIDRYPEEKDNNVLAWLGA 366
 QY 195 GSGIL---SFFAAQAGAR-KIYAVEASTMAQAEVLVKSNN---NLTDRIVVYIPGKVE 245
 Db 367 GGGPLVNASLRKAKQADRRIKILAYEKRNPA---VYTLNMQFEEMGSOYIVYSSDMRE 422
 QY 246 VSLPQVDIIIEPFGYMLFNEBMLESYLAKKYLKPSGMMFPITGIVHLPFTDEQLYM 305
 Db 423 WVAPEKADITVELLSGFSFADNELSPECLDGAQHFLDDGVISIGETSTFLAPLSSSKLVN 482
 QY 306 E-----QFTKANFRYQSPFHGVDSALRGAAVDEY-FRQPVYDTRDIRILMA 351
 Db 483 EVRACREKRDDEAOFEMEVYVRLHNFH--QLSAPQPCFTFSPHNRDPMID----- 531
 QY 352 KSVKTYVNLKLEKGGDLHRIIPKFMHLSGLVHGLAFWEDYAFGSIITVLSAPTE 411
 Db 532 -NNRYCT-----LEPPEVNT-----VLHGFAYFETVLYQDI-----TLSIR 568
 QY 412 PLTH-----WYQVRLCFOSPLFAKADTLGTCILLIAN-KROSDISIYAOV 457
 Db 569 PETHSPGMSWPIPLPIKQIPITVRGQITICVAFMCSNKKWYEMAYAPV 621
 RESULT 12
 T10666
 hypothetical protein F6E21.40 - Arabidopsis thaliana
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C>Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 16-Feb-2001
 C:Accession: T10666
 R:Bayan, M.; Lennard, N.; Quail, M.; Harris, B.; Rajandream, M.A.; Barrell, B.G.; Ban
 submitted to the protein sequence database, June 1999
 A:Reference number: Z16533
 A:Accession: T10666
 A:Molecule type: DNA
 A:Residues: 1-670 <BEV>
 A:Cross-references: EMBL:AL049914; GSPDB:GN00062; ATSP:F6E21.40
 A:Experimental source: cultivar Columbia; BAC clone F6E21
 C:Genetics:
 A:Gene: ATSP:F6E21.40
 A:Map position: 4
 A:Introns: 47/3; 87/1; 123/3; 203/3; 230/3; 255/3; 284/3; 305/1; 335/3; 347/3; 370/3;
 C:Superfamily: Schizosaccharomyces pombe negative regulator of mitosis skb1
 Query Match 5.1%; Score 163; DB 2; Length 670;
 Best Local Similarity 22.9%; Pred. No. 0.00038;
 Matches 80; Conservative 53; Mismatches 145; Indels 72; Gaps 11;
 QY 131 HTLERSV--FSRTESSAVQYQFYGYSGOONMM----- 164
 Db 293 HNLQRPLOSSSSGTEKRNPLRILDYVAIYLFQKESISEDERIELGRTDLPQAPLOPLMDN 352
 QY 165 -----QDYVRTGYQRAILQNHTE-FKDK-----IYLDVCGSGGIL---SFFA 203
 Db 353 LEAQTYETFERDSVXYIQORAVKALVDYRDEKASELTLYLMVYAGARGPLVRSALQ 412
 QY 204 AQAGAR--KIYAVEASTMA-QHAELVYKSNLTDRIIVYIPGKVEEYSLPQVDIIIESEP 260
 Db 413 AETDRKLKLYAVAEKNPNNAVVTLLHNLVKMEGMEVDVTTISCDMRFWNADEQADIIIVSELL 472

QY 261 GYMLFNERALSYLHAKKYLKPSGNMFPTIGDVHLAPFTDEQLYMEQFTKANFRYQPSFH 320
 DB 473 GSFQDNELSPEDLGNORLRLKPGDISIPSSYTFIQPITSKRLNDYKAKHDAHETAY 532
 QY 321 GVDLSALRGAAVDE---YRQPVVDFDIRILMAKSVKTYTNFLKAEKGDHLRIEIPKF 377
 DB 533 VKLHSLVAKLAPSOSEVFTTHPMFST-KVNNQRYKKLOFS---LPSDAG----- 577
 QY 378 HMLHSLVGLAFWPDVAFIGSIMTWLSTAPPEPLTHMYQVCLPSL 427
 DB 578 ---SALVHGFAGYFDSVLKYDVLHGLEPTTAPNMFSEPIFFPDKPV 623

RESULT 13

Conserved hypothetical protein MJ1452 - Methanococcus jannaschii
 C:Species: Methanococcus jannaschii
 C>Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 08-Oct-1999
 C:Accession: C64481
 R:Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blake,
 ; Reich, C.T.; Overbeek, R.; Kirkness, E.F.; Weinstock, K.G.; Merrick, J.M.; Glodek, A.;
 ; son, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A.
 Science 273, 1058-1073, 1996
 A:Authors: Kaine, B.P.; Borodovsky, M.; Kleen, H.P.; Fraser, C.M.; Smith, H.O.; Woese, C
 A>Title: Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii
 A:Reference number: A64300; MUID:96337999
 A:Accession: C64481
 A>Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-259 <BU>
 A:Cross-references: GB:U67586; GB:L77117; NID:g1592096; PIDN:AAB99463.1; PID:g1500335; T
 C:Genetics:
 A:Map position: FOR1422618-1423397
 C:Superfamily: Methanococcus jannaschii conserved hypothetical protein MJ1452; bioc home
 F:35-139/Domain: bioc homology <BIOC>

Query Match 4.6%; Score 146; DB 2; Length 259;
 Best Local Similarity 23.5%; Pred. No. 0.0017;

Matches 51; Conservative 48; Mismatches 78; Indels 40; Gaps 11;

QY 162 NMADYVRTGYORAILQNHDFDKIVLDVGGSGSLSPFAAQAARKIYAVEASTMA- 220
 DB 13 SLTDTYERLAFKNAI-ERVVD-EDDVFDLGTGSGILAMIAAKK-AKTYAIEILDPEFY 69
 QY 221 QHAEVLYKSNLNDRIYVIGKVEVSLPEQVDIIISEPMGYMFND---RMLESYLHAK 277
 DB 70 DYAKENIKVNGF-NNIEIIEGDASTYNFKEKADAVIAELDTALLIPEQYKVNMSIIE-R 127
 QY 278 KYLKPESGNMFP--TIGDVHLA-----FTDEQLYMEQFTKANFRYQPSFGVDLSALRG 329
 DB 128 GFLEKEDVKTIPAKAISTTQLEVKAKMSHIYDEDIKSEVSEVYIEVEVDHKTN----- 181
 QY 330 AAVDEYRQPVVDFDIRILMAKSVK-----YTV 358
 DB 182 -----PIEVSYNIELELEKSCENTLGIKRTYTI 209

RESULT 14

T25146
 hypothetical protein T23B5.1 - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
 C:Accession: T25146
 R:Percy, C.
 submitted to the EMBL Data Library, March 1997
 A:Reference number: T25146
 A:Accession: T25146
 A>Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-680 <WIL>
 A:Cross-references: EMBL:T293390; PIDN:CAB07676.1; CESP:T23B5.1
 A:Experimental source: clone T23B5

C:Genetics:
 A:Gene: CESP:T23B5.1
 A:Introns: 57/1; 149/3; 186/2; 272/3; 373/2; 428/3; 501/1; 618/3; 660/3

Query Match 4.4%; Score 138; DB 2; Length 680;
 Best Local Similarity 21.2%; Pred. No. 0.028;

Matches 66; Conservative 45; Mismatches 148; Indels 52; Gaps 10;

QY 163 MMDYVNTGYORAILQNHDFDKI--VLDVGGSGSLSPFAAQAARKIYAVEASTMA 220
 DB 145 MINDVKRNEFAKAL--NDT-IKSRITVDFDGGTGLSLAARKTNLVALENMCLT 201
 QY 221 QHAEVLYKSNLNDRIYVIGKVEVSLPEQVDIIISEPMGYMFNERMLESYLHAKYL 280
 DB 202 MISFEVLKRGVESRVNVAHKNSTYFETCEKADIVSETLDCVGEKIVETFLDAHVR 261
 QY 281 KPSGNMF-PTIGDVHLAPFTDEQLYMEQFTKANFRYQPSFGVDLSALR-----G 329
 DB 262 SHDRITFIPQATYVRLFSREIF-----DHICQYGGVRYRSEYKIGES 308
 QY 330 AAVDEYRQPVVDFDIRILMAKSVKTYTNFL-AKEDDLRIEIPFEHMLHSLVGL 388
 DB 309 DAEPYPCASADYSEFELSGVAMHSVDFSSIANLKSLSANSNFKIRPAKGVARGF 368
 QY 389 AFMPDVAFIG-----SITVW-LSTAPPEPLTHMYQVCLFQSPFLAKAGDTLSGTC 439
 DB 369 SVHETSLDTGHGDIIDSSKRAMDLGIIP-----FKPELVYCDKREYGSW 415
 QY 440 LLANKRQSYD 450
 DB 416 KILNNRDLVYN 426

RESULT 15

T41026
 probable methyltransferase - fission yeast (Schizosaccharomyces pombe)

C:Species: Schizosaccharomyces pombe
 C>Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 31-Jan-2000

C:Accession: T41026
 R:Kirrby, L.; Harris, D.; Wood, V.; Rajandream, M.A.; Barrell, B.G.

submitted to the EMBL Data Library, June 1998
 A:Reference number: T21965

A:Accession: T41026
 A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA
 A:Residues: 1-271 <MOR>

A:Cross-references: EMBL:AL023860; PIDN:CA119585.1; GSPDB:GN00068; SPDB:SPCC162.05
 A:Experimental source: strain 972h-; cosmid c162

C:Genetics:
 A:Gene: SPDB:SPCC162.05
 A:Map position: 3
 C:Superfamily: 3-demethylubiquitinone-9 3-O-methyltransferase; bioc homology

Query Match 3.9%; Score 123.5; DB 2; Length 271;
 Best Local Similarity 25.7%; Pred. No. 0.087;

Matches 47; Conservative 26; Mismatches 55; Indels 55; Gaps 9;

QY 155 GYLSOQON-----MMDYVRTG-----TYORAILQNHDFDK 187
 DB 20 GFLEQQRNHSVYVNEVDHFNELAKTWMWDGSRLLHLMNSTRLDPMFEVFERECFSGK 79
 QY 188 IVDVGGSGSLSPFAAQAARKIYAVEASTMA-----QHAEVLYKSNLNDRIYVIGK 242
 DB 80 KIIDIGGGGILISESMARLGA-SVAVDASPMALVAKHNSL---DVLNGRLTYIHGS 135
 QY 243 VEEVSLPEQVDII-----ISEPMGYMFNERMLESYLHAKKYLKPSGNM-PTIGDV 293
 DB 136 VEGSOLPTTFEDVYVCMVELEHVEQPDPLF---SLMEK-----VKPNGLVSTISRT 185
 QY 294 HLA 296
 ||

Thu Jun 21 08:07:40 2001

us-09-464-377-2.rpr

Page 7

Db 186 LLA 188

Search completed: June 20, 2001, 09:58:04
Job time: 178 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 20, 2001, 09:57:16 ; Search time 13.03 Seconds
(without alignments)
1598.414 Million cell updates/sec

Title: US-09-464-377-2

Sequence: 1 MAAAAATAGVPGAGSAGVAG.....PAISMASPMSTPTNTMHGSG 608

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 93435 segs, 34255486 residues

Total number of hits satisfying chosen parameters: 93435

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: SwissProt_39.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	494.5	15.6	353	ANM1_RAT	Q63009 rattus norv
2	494.5	15.6	371	ANM1_MOUSE	Q9J110 mus musculu
3	486	15.3	348	HMT1_YEAST	P38074 saccharomyc
4	484.5	15.3	334	ANM4_HUMAN	Q9NR22 homo sapien
5	481.5	15.2	361	ANM1_HUMAN	Q99873 homo sapien
6	475	15.0	448	ANM2_MOUSE	Q6R144 mus musculu
7	474.5	15.0	512	ANM3_HUMAN	Q60678 homo sapien
8	472.5	14.9	339	ANM1_SCHPO	Q9URX7 schizosacch
9	472	14.9	528	ANM3_RAT	Q70467 rattus norv
10	461	14.6	433	ANM2_HUMAN	P55345 homo sapien
11	123.5	3.9	271	COO3_SCHPO	Q74421 s hexapreny
12	122.5	3.9	638	K220_HUMAN	Q01546 homo sapien
13	120.5	3.8	1077	YBK1_YEAST	P38167 saccharomyc
14	119.5	3.8	827	YBY3_YEAST	P38274 saccharomyc
15	115	3.6	296	PRMA_HABIN	P44402 haemophilus
16	110	3.5	197	Y928_MERJA	Q58338 methanococc
17	109.5	3.5	311	PRMA_BACSU	P54460 bacillus su
18	108	3.4	355	CMAT_STRPE	Q06528 streptomyce
19	107.5	3.4	1289	C5AB_BACUD	Q45753 bacillus th
20	107	3.4	690	PTRB_MORLA	Q59536 moraxella 1
21	105	3.3	251	Y095_HABIN	Q57060 haemophilus
22	104.5	3.3	509	HOY1_YARLI	Q99160 yarrowia 11
23	103.5	3.3	300	PRMA_SYNY3	P73820 synecocyst
24	103.5	3.3	705	SYN1_HUMAN	P17600 homo sapien
25	103	3.3	656	DNL1_HELPY	Q25338 heliobacte
26	103	3.3	1281	YLB5_CAEEL	P47100 caenorhabdi
27	103	3.3	1755	YJZ9_YEAST	P47100 saccharomyc
28	102.5	3.2	191	YK51_ARCFU	Q28228 archaeeoglob
29	102.5	3.2	389	SERI_BOMBO	Q28228 bombyx mori
30	102.5	3.2	656	DNL1_HELPY	Q25338 heliobacte
31	102	3.2	880	BRC4_DROME	Q24206 drosophila
32	100	3.2	1472	A2MG_RAT	P66238 rattus norv
33	99.5	3.1	298	PRMA_CLOAB	P45558 clostridium

34	99.5	3.1	312	PRMA_STAUV	P45557 staphylococ
35	99	3.1	552	DCIP_ENTCL	P23234 enterobacte
36	98.5	3.1	596	HMEN_ANOGA	Q02491 anopheles g
37	98.5	3.1	3712	ACYS_CEPAC	P25464 cephalospor
38	98	3.1	477	ANM1_MOUSE	P11859 mus musculu
39	98	3.1	1505	CDE_HUMAN	P39880 homo sapien
40	98	3.1	1755	YJZ7_YEAST	P47098 saccharomyc
41	97.5	3.1	985	AGLU_ASPOK	Q12558 aspergillus
42	97.5	3.1	1148	ICER_PSEEX	Q30611 pseudomonas
43	97.5	3.1	706	PIB2_YEAST	Q03674 saccharomyc
44	97	3.1	750	MEI2_SCHPO	P08965 schizosacch
45	97	3.1	1286	AIDA_ECOLI	Q03155 escherichia

ALIGNMENTS

RESULT	ID	ANM1_RAT	STANDARD:	PRT:	353 AA.
AC	Q63009:				
DT	01-NOV-1997 (Rel. 35, Created)				
DT	01-NOV-1997 (Rel. 35, Last sequence update)				
DT	01-OCT-2000 (Rel. 40, Last annotation update)				
DE	PROTEIN ARGININE N-METHYLTRANSFERASE 1 (EC 2.1.1.-)				
GN	HRMT12 OR PRMT1.				
OS	Rattus norvegicus (Rat).				
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.				
OX	NCBI_TaxID=10116;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=96276999; PubMed=8663146;				
RA	Lan W.-J., Gary J.D., Yang M.C., Clarke S., Herschman H.R.;				
RT	"The mammalian immediate-early TIS21 protein and the				
RT	leukemia-associated Btg1 protein interact with a protein-arginine				
RT	N-methyltransferase."				
RL	J. Biol. Chem. 271:15034-15044(1996).				
CC	-1- FUNCTION: METHYLATES (MONO AND ASYMMETRIC DIMETHYLATION) THE				
CC	GUANIDINO NITROGENS OF ARGINYL RESIDUES PRESENT IN A GLYCINE AND				
CC	ARGININE-RICH DOMAIN (CAN METHYLATE HNRNP1 AND HISTONES).				
CC	-1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).				
CC	-1- TISSUE SPECIFICITY: URIDUTIOUS.				
CC	-1- SIMILARITY: BELONGS TO THE PROTEIN ARGININE N-METHYLTRANSFERASE				
CC	FAMILY.				
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration				
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -				
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CC	use by non-profit institutions as long as its content is in no way				
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CC	entities requires a license agreement (See http://www.isb-sdb.ch/announce/				
CC	or send an email to license@sdb-sdb.ch).				
CC	-----				
DR	EMBL; U60882; AAC52622.1; -				
KW	Transferase; Methyltransferase; Nuclear protein.				
SD	SEQUENCE 353 AA: 40522 MW; EDBB0587784CS27E CRC64;				
Query Match	15.6%; Score 494.5; DB 1; Length 353;				
Best Local Similarity	34.0%; Pred. No. 2.3e-29;				
Matches 115: Conservative 64; Mismatches 128; Indels 31; Gaps 7;					
QY	139 SRTTESSAVQ-----YQFYGYLSQOQNMADYRTTYQRAIQNHTDFDKIVLDV 192				
DB	18 AESSKPNVAEDMTSKDYFDSYAHFGIHEMLKDEKRTLYRNSMHNHLFDKVLVDV 77				
QY	193 GCGSIIILFFPAOAGARIVYEA STMADHAEVLVYNNLTGRIYVPGKVEEVSIP-DO 251				
DB	78 GSGTIIILFFPAKAKARIVYIEGCSISIDYAVIKANKLDHVVITIKKVEEVEIPVK 137				
QY	252 VDIISFPMGYMLFERNMLESTYIAK-KYLKPSGNMFTPTIGDVHLAPFTDEQLYMEQFTR 310				

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Db 138 VDIISEMVGCLFYESMNTVLAHARDKMLAPDGLIFPDRAITYATAIED-----ROYKD 192
Oy 311 ANFRIPSPSHGYDLSALKRAAVDEYRQPVDTEDIRIILMAKSVKYTVNLEAKEGDLHR 370
Db 193 YKIHWMENYVYGDMSCKIKVAI-----KEPLVDVADPKOLV-----TNACLLKEVDIYR 241
Oy 371 IRI-----PKRFHLSGLVHGLAFWFDVAFISIMVWISTAPDEPLTHYQVRCLE 423
Db 242 VVEDITFTSPFCLOVKKRNDVYALVAFNIEFTRCHKRTGFTSPSPSYTHMKQVTFY 301
Oy 424 OSPLFAKAGDTLSCGCLLIANKROSYDISIVAOVDTG 461
Db 302 EDYLVTKGEIEFTIGMRPNKNNDDLOFTDIDLEKG 339

RESULT 2
ANML_MOUSE
ID ANML_MOUSE STANDARD: PRT: 371 AA.
AC 09JTF0;
DT 01-OCT-2000 (Rel. 40, Created)
DT 01-OCT-2000 (Rel. 40, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE PROTEIN ARGININE N-METHYLTRANSFERASE 1 (EC 2.1.1.-).
GN HMTL12 OR PRMT1 OR MRMT1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20307889; PubMed=10848611;
RA Pawlak M.R., Scherer C.A., Chen J., Koshon M.J., Ruley H.E.;
RT "Arginine N-methyltransferase 1 is required for early postimplantation
mouse development, but cells deficient in the enzyme are viable.";
RL Mol. Cell. Biol. 20:4859-4869(2000).
CC -1- FUNCTION: METHYLATES (MONO AND ASYMMETRIC DIMETHYLATION) THE
GUANIDINO NITROGENS OF ARGINYL RESIDUES PRESENT IN A GLYCINE AND
ARGININE-RICH DOMAIN (CAN METHYLATE HNRNP1 AND HISTONES).
CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS: 1 (SHOWN HERE) AND 2; ARE
PRODUCED BY ALTERNATIVE SPLICING.
CC -1- SIMILARITY: BELONGS TO THE PROTEIN ARGININE N-METHYLTRANSFERASE
FAMILY.
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CC -----
DR EMBL; AF232716; AAF37292.1; -
DR EMBL; AF232717; AAF37293.1; -
DR MGD; MGI:107846; Hmtl12.
DR InterPro; IPR000051; -
DR Transferase; Methyltransferase; Nuclear protein; Alternative splicing.
FT VARSPIC 13 30 MISSING (IN ISOFORM 2);
SQ SEQUENCE 371 AA; 42435 MW; AEFCEF63001B1A58C CRC64;

Query Match 15.6%; Score 494.5; DB 1; Length 371;
Best Local Similarity 32.4%; Pred. No. 2,4e-29;
Matches 121; Conservative 67; Mismatches 149; Indels 37; Gaps 8;

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Oy 217 STMAOAEVLKSNLNRDRIYVIGKVEEYSLP-EGVDIIISEPMGYMLENERMLESTYH 275
Db 120 SSISDIAVKIYKANKLDHVVITIKGVEEVLPEKVDIIISEMVGCLFESMLNTVLAH 179
Oy 276 AK-KYLKPSGNMPEPTIGDVLHAPFTDEOLYMEQFTKANFRQPSFHGVDLSALGAANDE 334
Db 180 ARKKMLAPDGLIFPDRAITYATAIED-----ROYKDYKIHWMENYVYGDMSCKIKVAI-- 232
Oy 335 YRQPVVDFTDIRILMAKSVKYTVNLEAKEGDLHRIE-----PKRFHLSGLVHGL 387
Db 233 --KEPLVDVADPKOLV-----TNACLLKEVDIYTVKVEDLFTSPFCLOVKKRNDVYA 283
Oy 388 LAFWEDAFISIMVWISTAPDEPLTHYQVRCLEFSPLEAKGDTLSCGCLLIANKRO 447
Db 284 LVAFNIEFTRCHKRTGFTSPSPSYTHMKQVTFYMEDYLVTKGEIEFTIGMRPNKN 343
Oy 448 SYDISIVAOVDTG 461
Db 344 NRDLFTDIDLEKG 357

RESULT 3
HMTL_YEAST
ID HMTL_YEAST STANDARD: PRT: 348 AA.
AC P38074;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE HNRNP ARGININE N-METHYLTRANSFERASE (EC 2.1.1.-) (ODP1 PROTEIN).
GN HMT1 OR ODP1 OR RMT1 OR YBR034C OR YBR0320.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
OX NCBI_Taxid=4932;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=5288C;
RX MEDLINE=94378725; PubMed=8091864;
RA Smith P.H.M., de Haan M., Maat C., Grievell L.A.;
RT "The complete sequence of a 3.3 kb fragment on the right arm of
chromosome II from Saccharomyces cerevisiae reveals 16 open reading
frames, including ten open reading frames, five previously
identified genes and a homologue of the SCO1 gene.";
RL Yeast 10:S75-S80(1994).
RN [2]
RP SEQUENCE OF 1-55 FROM N.A.
RX MEDLINE=95204349; PubMed=7896706;
RA Loubardi A., Karst F., Guilloton M., Marchieau C.;
RT "sterol uptake induced by an impairment of pyridoxal phosphate
synthesis in Saccharomyces cerevisiae: cloning and sequencing of the
PX3 gene encoding pyridoxine (pyridoxamine) phosphate oxidase.";
RL J. Bacteriol. 177:1817-1823(1995).
RN [3]
RP CHARACTERIZATION.
RA Henry M.F., Silver P.A.;
RL Unpublished observations (MAR-1996).
RN [4]
RP CHARACTERIZATION.
RX MEDLINE=96218186; PubMed=8647869;
RA Gary J.D., Lin W.-J., Yang M.C., Herschmann H.R., Clarke S.;
RT "The predominant protein-arginine methyltransferase from
Saccharomyces cerevisiae.";
RL J. Biol. Chem. 271:12585-12594(1996).
CC -1- FUNCTION: METHYLATES ARGININES IN A VARIETY OF RNA-BINDING
PROTEINS. CAN CATALYZE BOTH THE MONO- AND ASYMMETRIC
DIMETHYLATION.
CC -1- SIMILARITY: BELONGS TO THE PROTEIN ARGININE N-METHYLTRANSFERASE
FAMILY.
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CC -----
DR EMBL; X76078; CAA53689.1; -
DR EMBL; Z35903; CAA84976.1; -
DR EMBL; X76992; CAA54296.1; -
DR PIR; S45890; S45890.
DR SGD; S0000238; HMT1.
KW Transferase; Methyltransferase.
SQ SEQUENCE 348 AA; 39786 MW; 363AF61033FB4AC2 CRC64;

Query Match 15.3%; Score 486; DB 1; Length 348;
Best Local Similarity 36.5%; Pred. No. 9,4e-29;
Matches 120; Conservative 56; Mismatches 121; Indels 32; Gaps 9;

QY 139 SEPTRESSAVV-YFOFYCYLSSQOQMMMDYVATGYORAILQNHDFDKIVLDVGGCGS 197
   ::::: | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 11 TEKRLTSSSEQHFFSYSDHYGHHEMLQDTVATLTSYRNAILQNKLFQDKIVLDVGGCGS 70
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 198 ILSPFAQAQARKIYAVEASTMAQHAEVLYKSNLTDRIYIPGVEEYSLP-ECVDIT 256
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 71 ILSMFAAHGKAHVIGVDMSSIIEMAKELVNGFSDKITTLRGLKEDVHLPFPYVDIT 130
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 257 SEPQCYLMEFNERMLESYLHAK-KYLKPSGNNMPTIGDVHLAFTDQLMEFTANRY 315
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 131 SEMMGYFLLYESMDQTVIYARDHYVEGGLFPPDKCSIHLAGLEP----SQKDEKINY 185
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 316 QPSFHVGLSLALRGAAVDEYFROPVDFEDIRILMAKSVKYVNFLEAK--EGDLHRIEI 373
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 186 WQDYVGFYSPR----VPLVLEHPYVDYE-----RNNVNTSSDKLIEFDLNTYKI 232
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 374 P-----FKFHMHSGLVHGIAFWDAVFG--SIMYWLSTAPTEPTLHWYQVRCLEQ 424
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 233 SDLAFKSNFKLAKRQDMINGIVTFDIYFPAPKGRKRPVEFSTGHPAPYTHWKQTFEPP 292
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 425 SPLFAKAGDTLSGTCOLLANKRQSDIS 453
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 293 DDLQAFETGDTLEGELVCSPEKERNRDLNI 321
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

RESULT 4
ANM4_HUMAN STANDARD; PRT; 334 AA.
AC Q9NR32;
DT 01-OCT-2000 (Rel. 40, Created)
DT 01-OCT-2000 (Rel. 40, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE PROTEIN ARGININE N-METHYLTRANSFERASE 4 (EC 2.1.1.-).
GN HMT1L3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Lorenz B., Strom T.M.;
RT "Transcripts in human map region 12p13.3."
RL Submitted (MAY-2000) to the EMBL/Genbank/DBJ databases.
CC -1- FUNCTION: PROBABLY METHYLATES THE GUANIDINO NITROGENS OF ARGINYL
CC RESIDUES IN SOME PROTEINS (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE PROTEIN ARGININE N-METHYLTRANSFERASE
CC FAMILY.
CC -----
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[illegible]

Submitted (Jan-2000) to the EMBL/GenBank/DBJ databases.

-1- FUNCTION: METHYLATES (MONO AND ASYMMETRIC DIMETHYLATION) THE GUANIDINO NITROGENS OF ARGINYL RESIDUES PRESENT IN A GLYCINE AND ARGININE-RICH DOMAIN (CAN METHYLATE HNRNAI AND HISTONES) (BY SIMILARITY).

-1- SUBCELLULAR LOCATION: NUCLEAR.

-1- ALTERNATIVE PRODUCTS: 3 ISOFORMS; 1/2 (SHOWN HERE), 2/3 AND 3/4; ARE PRODUCED BY ALTERNATIVE SPLICING.

-1- SIMILARITY: BELONGS TO THE PROTEIN ARGININE N-METHYLTRANSFERASE FAMILY.

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DR EMBL; Y10806; CAA71764.1; -
 DR EMBL; Y10805; CAA71763.1; -
 DR EMBL; Y10807; CAA71765.1; -
 DR EMBL; D66904; BAA11029.1; -
 DR EMBL; AF222689; AAF62893.1; -
 DR EMBL; AF222689; AAF62894.1; -
 DR EMBL; AF222689; AAF62895.1; -
 DR MIM; 602950; -
 KW transferase; Methyltransferase; Nuclear protein; Alternative splicing.
 FT VARSPPLIC 1 19 MENFVATLANGMSLOPPE -> MGVVA (IN ISOFORM 2).
 FT FT 18 108 V -> E (IN ISOFORM 3).
 FT CONFLICT 147 175 DIITSEMGTCLEYESMLNLYVARDKWL -> ASSASGCM
 FT FT AATSTSPGCTPCSMGTSV (IN REF. 2).
 FT SEQUENCE 361 AA; 41485 MW; A288969B5AF8760 CRC64;

Query Match 15.2%; Score 481.5; DB 1; Length 361;
 Best Local Similarity 31.8%; Pred. No. 2.1e-28;
 Matches 119; Conservative 68; Mismatches 150; Indels 37; Gaps 8;

QY 97 GSFIITLGCNSVLIQFATPHDFCSFYNIILKTCRGHTLERSVFSEPTRESSAVOYFOFGY 156
 DB 2 ENFVALI-ANGMSLOPPELEVSG-----QASESEKPAEMEMTKDYFDSTYAH 49

QY 157 LEOQONMODYVFTGYQRAIIQNHDFDKIVLDVGGSGIISFPAQAQARRIVAEA 216
 DB 50 FGIHEMLKDEVTLYRNSMFHNRHLFKDKVLDVGGSGIILCPAARAKARVIGIYC 109

QY 217 STMAQAEVLVKNLNDLRIVIPGKVEEVLSP-EQVDIITSEPMGYMLFNERMLESTYLH 275
 DB 110 SSISDVAIVKIKLNDHVVTIIGKVEEVELPEKVDIITISEMGYCLYESMLNLYV 169

QY 276 AK-KYLKPSGNMPTIGDVHIAFTDEQLMEQFTKANFRQPSFHVDSALGAAVDE 334
 DB 170 ARKMLAPDGLIFPDRLTYIAED-----ROYKDKIIMWENVYGFDSCLIDVAI-- 222

QY 335 YFQPVVDFFDIRILMAKSVKYTVNLEAKEGDLRIE-----DFKEMHLSGLVHG 387
 DB 223 --KEPLVDVVDPKOLV-----TNACLIKEDVIYKVEDLFTSPCLQVKNRNDYVA 273

QY 388 LAWEVDVAPIGSLMTYWLSTAPTEPLTHYQVRCLEFSPFAKGDPLSGCLLIANKRQ 447
 DB 274 LVAVFNIIEFRCRKRGTGSPSPSYHMKQVTFYMEDYLVTKGEIIFGTIGMRPAKN 333

QY 448 SYDISIYAOVDGTG 461
 DB 334 NRDLFTDIDFGK 347

RESULT 6
 ANM2 MOUSE STANDARD; PRT; 448 AA.
 ID ANM2_MOUSE

AC G9R144;
 DT 01-OCT-2000 (Rel. 40; Created)
 DT 01-OCT-2000 (Rel. 40; Last sequence update)
 DT 01-OCT-2000 (Rel. 40; Last annotation update)
 DE PROTEIN ARGININE N-METHYLTRANSFERASE 2 (EC 2.1.1.-).
 GN HMTLLI OR PRMT2.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Tavba L.O., Kvasna S.M., Skripkina I.Y., Anoprienko O.V., Slavov D.,
 RA Tassone F., Rynditch A.V., Gardiner K.;
 RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: PROBABLY METHYLATES THE GUANIDINO NITROGENS OF ARGINYL
 CC RESIDUES IN SOME PROTEINS (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE PROTEIN ARGININE N-METHYLTRANSFERASE
 CC FAMILY.
 CC -1- SIMILARITY: CONTAINS 1 SH3 DOMAIN.

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DR EMBL; AF169620; AAD4847.1; -
 DR MGD; MGI:131652; Hmtll1.
 DR HSP; P06241; ISH.
 DR InterPro; IPR000051; -
 DR InterPro; IPR001452; -
 DR PRINTS; PR00452; SH3DOMAIN.
 DR PROSITE; PS50002; SH3; 1.
 KW transferase; Methyltransferase; SH3 domain.
 FT DOMAIN 42 101 SH3.
 FT SEQUENCE 448 AA; 50476 MW; 63E1F8C3FC66C25E CRC64;

Query Match 15.0%; Score 475; DB 1; Length 448;
 Best Local Similarity 31.0%; Pred. No. 8.8e-28;
 Matches 138; Conservative 64; Mismatches 171; Indels 72; Gaps 14;

QY 23 GAGPCATVVFPGARLLTIGDANGELIORHAPQALRLERAGPDAAGIALISHVEYCVFK 82
 DB 5 GEGCSESQVLP---VLEEDVDVGCCEMQLQDQLOLOLOPE-----EFVAIAD 52

QY 83 CSVRETECSHVGROSFTITLGCNSVLIQFAPPHDFCSFYNIILKTCRGHTLERSVFSEPT 142
 DB 53 YTADEDTOLS-----FLRGEKILLRQTTADM--WNGERACCGY-IPANILGKOL 100

QY 143 EESSA-----VOYFOFGYLSOOONMADYVFTGYQRAIIQNHDFDKIVLDVGGSGS 196
 DB 101 EYDPEDTWOBEYFDSTGLKHLHMLADQRTKYHSVILQNNESLKDXYLIDVGGCT 160

QY 197 GILSFPAA-QAGARKIVAEASTMAQHAELVYKSNLNDLRIVIPGKVEEVLPEQVDII 255
 DB 161 GIIISLFCNHHARPRAYVAEASDMAQHTSQLVQNGFADTIIVFOOKVEDVVLPEKVDVL 220

QY 256 ISEPMGYLTFNERMLESYLAK-KYLKPSGNMPTIGDVHIAFTDEQLYMGOFKRNKR 314
 DB 221 VSENMGTCLLEFMEISLIVARDTWLKGDIITPTAALHVLPCSAEKDYHSKVLFMDNA 280

QY 315 YQSFHGVDSLALGAAVDEYFROP-----VVDFFDIRILMAKSVKYTV 358
 DB 281 YE-----FNLSAKSLAKIEFSPSRKSNHLKPEDCLSEPCITLIDDMHTVG-----V 328

QY 359 NFLAKEGDLRIEIPKFNHLSGLVGLAFWDVAF-----IGSIMYWLSTAPTEPLT 414
 DB 329 PDLEMRGEL-----RFDIQAGTGLHGTAFWESVYFQSLREGOPQOV-VSTGLHPPT 380

OY 445 KROSYDISI 453
DB 309 NHRELDIDI 317

RESULT 9

ANM3_RAT STANDARD; PRT: 528 AA.

AC 070467;
DT 01-OCT-2000 (Rel. 40, Created)
DT 01-OCT-2000 (Rel. 40, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE PROTEIN ARGININE N-METHYLTRANSFERASE 3 (EC 2.1.1.-).

OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;

RP SEQUENCE FROM N.A.
RX MEDLINE=98307932; PubMed=9642256;

RA Tang J., Gary J.D., Clarke S., Herschman H.R.;
RT "PRMT 3, a type I protein arginine N-methyltransferase that differs
RT from PRMT1 in its oligomerization, subcellular localization,
RT substrate specificity, and regulation.";

RL J. Biol. Chem. 273:16935-16945(1998).

CC -1- FUNCTION: METHYLATES (MONO AND ASYMMETRIC DIMETHYLATION) THE
CC GUANIDINO NITROGENS OF ARGINYL RESIDUES IN SOME PROTEINS.

CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC.

CC -1- SIMILARITY: BELONGS TO THE PROTEIN ARGININE N-METHYLTRANSFERASE
CC FAMILY.

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CC or send an email to license@sib-sib.ch).

CC EMBL: AF059530; AAC40158.1; -

DR InterPro: IPR000051; -

DR InterPro: IPR000822; -

DR PROSITE: PS00028; ZINC_FINGER_C2H2; UNKNOWN_1.

KM Transferase; Methyltransferase; Zinc-finger.

FT ZN.FING 46 69 C2H2-TYPE.

SO SEQUENCE 528 AA; 59419 MW; B25D627902594B39 CRC64;

Query Match 14.9%; Score 472; DB 1; Length 528;
Best Local Similarity 34.2%; Pred. No. 1.9e-27;
Matches 123; Conservative 63; Mismatches 140; Indels 34; Gaps 11;

OY 111 OFATPHDFCSFYILKTCRGTLSRVSESTRESSAVOFEFGYLSOOONMMQDVVRI 170
DB 186 QRA--QDFVNAVUV-KTCSST---TIALQDEDEGV-YFSSYGHGHEEMAKDKVRI 237
OY 171 GYVRAAILNHTDFKDKIVLDCGSGSILSFPAAGARRIYVEASTMAQHAELVKN 230
DB 238 ESTRDITVYQNPFIKDKVYLDVCGCGSILSMFAKAKKIVINVDSEILLYQANDIIRLN 297
OY 231 NLTDRIVIPGKVEVSLP-EQVDIIISDPGYLLENRMLESYLAK-KYLKPSGMFP 288
DB 298 KLEDTIVLJKGLEEVSLEPEKVDVISEMVGFLFEESMLDSVLYAKSKYLAKGSGSYVP 357
OY 289 TIGDVALAPFTDQLYMEQCTKANFRQPSFHGVDSALGAVNDEFRQPVDTFDIRI 346
DB 358 DICTISLVAVSDSKADRIA-----FWDVYGFNMSCMKKAVTPE---AVEEVVHK 408
OY 349 LMAKSVKYVNFLEAKGDLRIE-----PFKFMHLSGLVHGLAFWDFVAFISIM 401
DB 409 LISDP-----CDIKIHCHTISISDLERSSDFTLTTRTAMCTAVAGFDIIFKRNCH 461

OY 402 T-VMLSNAPTEPLTHWQVRCFLFSPFAKAGDLSGTCLLIANKROSYDISIAVOVDOT 460
DB 462 NRYVSTGPOSTKTHMKQITFLLEKPPYKAGELKKTIVHKKKDPRLIVLTINSS 521

RESULT 10

ANM2_HUMAN STANDARD; PRT: 433 AA.

AC P53345; P78350; Q9UMC2;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE PROTEIN ARGININE N-METHYLTRANSFERASE 2 (EC 2.1.1.-).

OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;

RP SEQUENCE FROM N.A.
RX MEDLINE=98207248; PubMed=9545638;

RA Scott H.S., Antonarakis S.E., Lalioti M.D., Rossier C., Silver P.A.,
RA Henry M.F.;
RT "Identification and characterization of two putative human arginine
RT methyltransferases (HRMT1L and HRMT1L2).";

RL Genomics 48:330-340(1998).

CC -1- FUNCTION: METHYLATES (MONO AND ASYMMETRIC DIMETHYLATION) THE
CC GUANIDINO NITROGENS OF ARGINYL RESIDUES IN SOME PROTEINS.

CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC.

CC -1- SIMILARITY: BELONGS TO THE PROTEIN ARGININE N-METHYLTRANSFERASE
CC FAMILY.

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CC or send an email to license@sib-sib.ch).

CC EMBL: X99209; CA67599.1; -

DR EMBL: U080213; AAB48437.1; -

DR EMBL: AL109794; CAB52454.1; -

DR HSSP: P06241; 1A2G.

DR MIM: 601961; -

DR InterPro: IPR001452; -

DR Pfam: PF00018; SH3.1.

DR PRINTS: PR00452; SH3DOMAIN.

DR PROSITE: PS50002; SH3.1.

KM Transferase; Methyltransferase; SH3 domain.

FT DOMAIN 30 89 SH3.

FT CONFICT 256 260 KDYS -> RIVA (IN REF. 2).

SO SEQUENCE 433 AA; 49041 MW; 6DEB0350C15CD4F CRC64;

Query Match 14.6%; Score 461; DB 1; Length 433;
Best Local Similarity 34.7%; Pred. No. 9.1e-27;
Matches 119; Conservative 53; Mismatches 123; Indels 48; Gaps 10;

OY 402 T-VMLSNAPTEPLTHWQVRCFLFSPFAKAGDLSGTCLLIANKROSYDISIAVOVDOT 460
DB 462 NRYVSTGPOSTKTHMKQITFLLEKPPYKAGELKKTIVHKKKDPRLIVLTINSS 521

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QY 149 QYFQFYGLSQQQMMDDYVYTGTYGABALIONHDFDKIYVLVGGSGILSFEAAQ-AG 267
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 101 EYFSGYGLKHLHMLADOPRTTYTHSYVILONKSLTDKCYLIDVGGCGTGLISLCAIYAR 160
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 208 ARKIYAVEASTMAOHAELYKSNMLDRIYVIPKVEEVALPEVDIISIEPMGYMLFNE 267
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 161 PRAYAAVEASMAOHTGQVLYLONFALITYYQOKVEDVYLPEKVNDVLYSEMGKTCILFE 220
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 268 RMLESYLHAK-KYLPKSGNNEPPTIGDVHLAPETDEOLYMOFTKANRYOPSFGYDLSA 326
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 221 FMESILYARDAWMLKEGVIMPTMAALHLVPCSDAKDY-----RSKULFMDNMYEENLSA 275
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 327 LRGAANDYEFQOP-----VDFDILIMAKSVKYTVNLFLEAKEGDLAR 370
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 276 LKSLAVEEFESPKPYNHILKPEDCLSEPTYLIDQMTWVO-----ISDLETLRSEL- 326
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 371 IEIPFKFMHLHSGVHGLAEFDVAF-----IGSIMTWLSTAPTEPLTHYQVRCLEFOS 426
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 327 -----REDIRKAGTLHGFYAFESVHFSLOEGORPOV-ISTGRPHNPTWKKOFLFMDDP 380
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 427 LEAKAGDLSGTCLLIN---KRQSYDIS--IYAOVDGYSK 463
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 381 VPVHTGDVYIGSVYLOKRNPMYRKRMSVATLSMAVTSRKDDPFSOK 423

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Query Match      3.9%; Score 123.5; DB 1; Length 271;
Best Local Similarity 25.7%; Pred. No. 0.045;
Matches 47; Conservative 26; Mismatches 55; Indels 55; Gaps 9.

QY 155 GYLSSQGN-----MMQDYVRTG-----TYQRAIIQNHDFDKD 187
      |||||: : : : :
Db 20 GFLSQQRHNSVSYNEVDHFNELAKTWMDMGDSRLHLNSTRDPMTEVEFRNCFSGK 79
      :|||:|||||: :|||:|||||: :|||:|||||: :|||:|||||:
QY 188 IYLDVGGCCSGILSPFAAAGARKITAVVASTYA-----QHAELVLYKSNLDRIVYISGK 242
      :|||:|||||:|||||: :|||:|||||: :|||:|||||: :|||:|||||:
Db 80 KILDGCGGGILISESMARLGA-SYTAVYASPAIIVAKKHAQL--DPLMGRLEYIGGS 135
      :|||:|||||:|||||: :|||:|||||: :|||:|||||: :|||:|||||:
QY 243 VEEVSLPEQVQII-----ISEPMGYLFEFMRMLESYLHAKKYLKPSGNM-PEPTIGDV 293
      |||||: :|||:|||||: :|||:|||||: :|||:|||||: :|||:|||||:
Db 136 VEGSLPLPTTFDVIYVCMEVLHVEHQRPDLF--SLMER-----VKRNGRLVLTISRT 185
      |||||: :|||:|||||: :|||:|||||: :|||:|||||: :|||:|||||:
QY 294 HLA 296
      |||||
Db 186 LLA 188

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QY 149 QYFQFYGLSQQQMMDDYVATGTYGABALIONHDFDKIYLDVGGSSGLTSEFAAQ-AG 267
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 101 EYFSGYGLKHLHMLADOPRTTYTHSYVILONKNSLTDKCYLIDVGGCGTGLTSLCAIYAR 160
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 208 ARKIYAVEASTMAOHAELYKSNMLDRIYVIPKVEEVALPEVDIIESEPGMYLFE 267
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 161 PRAYAAVEASMAOHTGQVLYONFALITYOQKVEDVYLPEKVDVLYSEMGKTCILFE 220
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 268 RMLESYLHAK-KYLPKSGNNEPTIGDVHLAPETDEOLYMOFTKANRYOPSFGYDLSA 326
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 221 FMESILYARDAMLKEDGVIMPTMAALHLVPCSDAKDY-----RSKULFMDNMYEENLSA 275
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 327 LRGAANDEYFQOP-----VDFDILIMAKSVKTYVNFLEAKEGDLAR 370
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 276 LKSLAVEEFESPKPYNHILKPEDCLSEPTYLIDQMTWVO-----ISDLETLRSEL 326
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 371 IEIPFKFMHLHSGVHGLAEFDVAE-----IGSIMTWLSTAPTEPLTHYQYRCLEFOS 426
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 327 -----REDIRKAGTLHGFYAFESVHFSLOEGORPOV-ISTGRPHNPTWKKOFLFMDDP 380
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 427 LEAKAGDLSGTCLLIAN---KRQSYDIS--IYAQVDGFSK 463
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 381 VPVHTGDVYIGSVYLOKRNPMYRRKRMASVALSMAYTSKDDPFSOK 423

```

```

Query Match      3.9%; Score 123.5; DB 1; Length 271;
Best Local Similarity 25.7%; Pred. No. 0.045;
Matches 47; Conservative 26; Mismatches 55; Indels 55; Gaps 9.

QY 155 GYLSSQGN-----MMQDYVRTG-----TYQRAIIQNHDFDKD 187
      |||||: : : : :
Db 20 GFLSQQRHNSVSYNEVDHFNELAKTWMDMGDSRLHLNSTRDPMTEVEFRNCFSGK 79
      :|||:|||||: :|||:|||||: :|||:|||||: :|||:|||||:
QY 188 IYLDVGGCCSGILSPFAAAGARKITAVVASTYA-----QHAELVLYKSNLDRIVYISGK 242
      :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 80 KILDIGCGGGLISESMARLGA-SYTAIVASPAIIVAKKHAQL--DPLMGRLEYIGGS 135
      :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 243 VEEVSLPEQVQII-----ISEPMGYLFEHRLAESYLIHAKKYLKPSGNM-PTIGDPV 293
      |||||: :|||:|||||: :|||:|||||: :|||:|||||: :|||:|||||:
Db 136 VEGSLPLPTTFDVVICMEVLEHVEQRPDLF--SLMER-----VKRNGRLVLTISRT 185
      |||||: :|||:|||||: :|||:|||||: :|||:|||||: :|||:|||||:
QY 294 HLA 296
      |||||
Db 186 LLA 188

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QY 181 HTDKRIVLVGGSGITLSPFAAQAQARKIYAVEASTMAOHAELYVKSNNLTDRIVIP 240
DB 181 HTDKRIVLVGGSGITLSPFAAQAQARKIYAVEASTMAOHAELYVKSNNLTDRIVIP 240
QY 241 GKVEEVSLEPEQVDIIISPEPMYLFENEMLESYLAKKYLKPCGNMPTIGDVHLAPFD 300
DB 241 GKVEEVSLEPEQVDIIISPEPMYLFENEMLESYLAKKYLKPCGNMPTIGDVHLAPFD 300
QY 301 EQLYMEQFTKRNFRQSPFHGVDLSALGAADVDEYFROPVDTFDIRILMAKSVKYTVNF 360
DB 301 EQLYMEQFTKRNFRQSPFHGVDLSALGAADVDEYFROPVDTFDIRILMAKSVKYTVNF 360
QY 361 LEAKEGDHRLEIFPKFMLHSGVLHGALFMPDVAFIGSIMTWLSTAPTEPLTHWYOR 420
DB 361 LEAKEGDHRLEIFPKFMLHSGVLHGALFMPDVAFIGSIMTWLSTAPTEPLTHWYOR 420
QY 421 CLFQSPLEFAKAGDITLSTCLLIANKRQSYDISIYAVODQTSKSNLLDKNPFRTYGT 480
DB 421 CLFQSPLEFAKAGDITLSTCLLIANKRQSYDISIYAVODQTSKSNLLDKNPFRTYGT 480
QY 481 TPSPPPSGHITSPEENMNTGSTYLSGVAVAMPYADLSSVYAGSSVGHNLPLA 540
DB 481 TPSPPPSGHITSPEENMNTGSTYLSGVAVAMPYADLSSVYAGSSVGHNLPLA 540
QY 541 NTGIYVNHSHRMSGIMSTGIYOGSSGAOGSSSAHYAVNNQFTMGPAISMASPMSP 600
DB 541 NTGIYVNHSHRMSGIMSTGIYOGSSGAOGSSSAHYAVNNQFTMGPAISMASPMSP 600
QY 601 TMTMHYS 608
DB 601 TMTMHYS 608

RESULT 2
QYVH48
AC 09VH48 PRELIMINARY; PRT; 530 AA.
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-JUN-2000 (TREMBlrel. 14, Last annotation update)
DE C5358 PROTEIN.
GN C5358.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidae; Drosophilidae; Drosophila.
OC NCBITaxID=7227;
RN
RP SEQUENCE FROM N.A.
RC STRAIN=BERKELEY.
RA MEDLINE-20196006; PubMed-10731132.
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Mortman J.R., Yandell M.D., Zhang O., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abille J.F., Agbayani A., An H.-J., Andrews-Pfankoch C., Baldwin D.,
RA Balley R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasly E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brothier P.,
RA Butts K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Dudin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hotal J.D., Houston K.A., Howland T.J., Wei M.-H., Ibeagwu C.,
RA Jaisli M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Kethum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,

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RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Mekulov G., Milshina N.V., Modarri C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon R., Nusskern D.R., Pacle J.M.,
RA Palazolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shie B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spler E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svrtkas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Welnslock G.M., Welssendach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhan G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,
RT "The genome sequence of Drosophila melanogaster."
RL Science 287:2185-2195(2000).
DR EMBL; AE003685; AAF54471.1; -.
DR Flybase; FBgn0037770; C5358.
DR InterPro; IPR000051; -.
SQ SEQUENCE 530 AA; 59727 MW; 61590959D6B91EEA CRC64;

Query Match 44.5%; Score 1409; DB 5; Length 530;
Best Local Similarity 59.3%; Pred. No. 2,4e-103;
Matches 264; Conservative 74; Mismatches 99; Indels 8; Gaps 2;

QY 85 VSRETECSVVGQSFITLIGCNLSVLIQFATPHDFGFIYILCTCRHTLEKRSYFSEKTEE 144
DB 80 IADPDAQOMGRSVAVSLADNLVLFASQDQQLFRFVENVK-HLRKVSFSGRTSE 138
QY 145 SSAVGYFQFYGLTSGQNNMODYVRTGYQRAILQNHTEFKRIVLDVCGSGITLFFFA 204
DB 139 SSASQFQFYGLTSGQNNMODYVRTGYQRAILQNHTEFKRIVLDVCGSGITLFFFA 198
QY 205 QAGARKIYAVEASTMAOHAELYVKSNNLTDRIVIPGKVEEVSLEPEQVDIIISPEPMY 264
DB 199 QAGARKIYAVEASTMAOHAELYVKSNNLTDRIVIPGKVEEVSLEPEQVDIIISPEPMY 258
QY 265 FNEBMEESTLAKKYLKPCGNMPTIGDVHLAPFDQOLYMEFTANFRYQSPFHGYDL 324
DB 259 YNERMLETYLHARKWLKPGKMYPTHGDLHIAFSDSELSYSEQYNANFWQSAFHYGVDL 318
QY 325 SALRGAADVDEYFROPVDTFDIRILMAKSVKYTVNFLEAKEGDHRLEIFPKFMLHSG 384
DB 319 TILHEKMEKYEIRQPLVDTFDIRILMAKSVKYTVNFLEAKEGDHRLEIFPKFMLHSG 378
QY 385 VGLAFMPDVAFIGSIMTWLSTAPTEPLTHWYORCLFQSPLEFAKAGDITLSTCLLIAN 444
DB 379 CHGLAFMPDVAFIGSIMTWLSTAPTEPLTHWYORCLFQSPLEFAKAGDITLSTCLLIAN 438
QY 445 KROSVDISIVAOVDQTSKSNLLDKNPFRTYGTTPSPPPSGHITSPEENMNTGSTYLS 498
DB 439 KROSVDISIVAOVDQTSKSNLLDKNPFRTYGTTPSPPPSGHITSPEENMNTGSTYLS 498
QY 499 -NTGSTYLSGVAVAMPYADLSSVYAGSSVGHNLPLA 542
DB 499 GSRNSSMLNGISVNGIGEGMDIT 523

RESULT 3
QYVH06
AC 09VH06 PRELIMINARY; PRT; 388 AA.
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
DE PUTATIVE ARGININE METHYLTRANSFERASE.
GN F17A9.8
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC Magnoliophyta; eudicotyledons; core eudicot; Rosidae; eurosids II;
OC Brassicales; Brassicaceae; Arabidopsis.
OC NCBITaxID=3702;

```

Query Match	27.3%;	Score 864.5;	DB 10;	Length 577
Best Local Similarity	38.7%;	Pred. No. 4.3e-60;		

```

RESULT      5
09SU94
ID      09SU94      PRELIMINARY;      PRI;      390 AA.
AC      09SU94;
DT      01-MAY-2000 (TREMBLrel. 13, Created)
DT      01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT      01-OCT-2000 (TREMBLrel. 15, last annotation update)
DE      ARGININE METHYLTRANSFERASE (PAM1).
GN      T16L4.20 OR AT4G299510.
OS      Arabidopsis thaliana (Mouse-ear cress).
OC      Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC      Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
OC      Brassicales; Brassicaceae; Arabidopsids.
OX      NCBI_TaxID=3702;
RN      [1]
RP      SEQUENCE FROM N.A.
RA      Bevan M., Rose M., Hempel S., Entlan K.-D., Bancroft I., Mewes H.W.,
RA      Mayer K.F.X., Lemcke K., Schueller C.;
RL      Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
RN      [2]
RP      SEQUENCE FROM N.A.
RA      EU Arabidopsis sequencing project;
RL      Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
RN      [3]
RP      SEQUENCE FROM N.A.
RA      Rose M., Hempel S., Entlan K.-D., Mewes H.W., Lemcke K., Mayer K.F.X.;
RL      Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN      [4]
RP      SEQUENCE FROM N.A.
RA      EU Arabidopsis sequencing project;
RL      Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR      EMBL; AL079344; CAB45311.1; -
DR      EMBL; AL161575; CAB979709.1; -
DR      InterPro; IPR000051; -

```


Query Matchc 14.3%; Score 453.5; DB 5; Length 355;
Best Local Similarity 33.8%; Pred. No. 7.9e-28;
Matches 117; Conservative 66; Mismatches 130; Indels 33; Gaps 10;

QY 131 HTLSEVSESRFESSAVOYFOFYGYLSOOOMMODVYATGTYORALIONHDFKDKIVL 190
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Dd HHDANQIINKDRROGE--HYFKLYGRIEIHLEWLLDSVRKAYRKAEL-QHNFFRKRYVL 72
QY 191 DVGCGSGLISFPAADAGARKIYAVEASTMAOAHAELYVKSNNITDRIWIPIGVEEVSLE 250
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Dd DVGCGMGVLSMFAAKAGSKRVLAEEAATISEFAAOOVODNEFGRAVIQVIGCVEDIELPD 132
QY 251 ---OVDIIISEMGMLNERNLESTYLAK-YLKPSGMFPETIGDIHAP--TDOLX 304
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 133 GIKKVIDIICDMWGSCLESIGNMESLPLPRKDMSLATGHITDYTAQLYIAAIKRDDVL- 191
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 305 MEQFTKANFRYOPSPFHGVDSLALR---GAADEYFRQPVVDTPDIRILMAKSVK-YTVN 359
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Dd 192 -----GFHWIDHGFDLSAIRRCESKAVEHV---TSGQMMSRVCLVKSIDLTYEP 239
QY 360 FLEAEGLHRLEIPFKRHMLSHGLVHLAFEDVAFLGISITFWLSTAPEPDLTHWYOV 419
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Dd 240 ROSASRSRL-----FELKVSNGRWGHGVAFDVGFSGKTQRISFTSPSPAPTHMNQT 293
QY 420 ROLFOSPLFAKAGDTLGGTCILLANKROSYSITSIAOVQDGSKSS 465
Db 294 VFYLETLPVPRAGETCKGVLTKKPSDESLTFDETDFIVNFDEREKS 339

RESULT 12
Q9NVNR ID Q9NVNR PRELIMITARY: PRT: 316 AA.
AC 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE CDNA FLJ10559 FIS, CLONE NT2R2002618, WEAKLY SIMILAR TO PROTEIN
DE ARGININE N-METHYLTRANSFERASE 2 (EC 2.1.1.-).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
NCBI_Taxid=9606;
[1]
RN XN
RP SEQUENCE FROM N.A.
RA Itogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,
RA Nishikawa T., Nagai K., Sugano S., Takahashi-Fujii A., Hara H.,
RA Tanase T., Nomura Y., Togiya S., Komai Y., Hara R., Takeuchi K.,
RA Arita M., Nabekura T., Ishii S., Kawai Y., Saito K., Yamamoto J.,
RA Wakamatsu A., Nakamura Y., Nagahari K., Masuo Y., Oshima A.,
RT "MEDO human cDNA sequencing project."
RL Submitted (FEB-2000) to the EMBL/Genebank/DBJ databases.
DR EMBL, AK01421; BAA91681.1; -
DR InterPro; IPR000051; -
SQ SEQUENCE 316 AA; 35238 MW; E35E5567C2EA80E CRC64;

Query Match 14.3%; Score 452.5; DB 4; Length 316;
Best Local Similarity 38.1%; Pred. No. 7.9e-28;
Matches 117; Conservative 39; Mismatches 108; Indels 43; Gaps 8;

QY 163 MMQDYVRGTGYRALIONHTDPKDKIVLDVCGCGSGLISFPAADAGARKIYAVEASTMAOH 222
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Dd 1 MADVRVTRDAYRLGIIRMMALRGVTYLDVGAGTGSLIFCAOGARRVAYAEASAIIWOQ 60
QY 223 AEVLKSNUNLDRIVIVIPCKVEEVSLEPOVDIIISEPMGYLFNERMLESTYLAK-KYKL 281
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Dd 61 AREVVRENGLEDERVAHPVETVELPEQVDIVSEMKGTLGHESMSSLVHAARKWLK 120
QY 282 PSGNPFPTIGDVHLAPFTDEQLYMEQFTKANFRYOPSFH-GVDSLALRGAAVDEYFRQPV 340
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Dd 121 EGGLLPPASAEFLIAPISQMLEM-----RLGRMSQVKQHGYVDMSCLES----- 165
QY 341 VDFPIRILMAKSVKYTVNVEAKES-----DLHRIELP-----EFKEML 380

Dd	166	--FATRLMGHS-EIVVQISGSEVDLARPOFOALELSRACLEDELEAGVGRRRCSTY	221
Qy	381	HSGLVHGLAFMEDVAFIG-SIMTWLSTARPEPLTHWYOVCLEPSPFLAKAGDTLSTG	438
Dd	222	GSAPRHGAIFNQYTFEGESEKPLVLSTSPPHATHTMKQALLYLNEPVQVQRDIDVSGE	281
Qy	439	CCLTANK 445 :::	
Dd	282	ITLLPSR 288	
RESULT 13			
ID	Q9SNQ2	PRELIMINARY;	PRT; 380 AA.
AC	Q9SNQ2;		
Dt	01-MAY-2000 (TREMBLrel, 13, Created)		
Dt	01-MAY-2000 (TREMBLrel, 13, Last sequence update)		
Dt	01-MAY-2001 (TREMBLrel, 16, Last annotation update)		
De	SIMILAR TO PROTEIN ARGININE N-METHYL TRANSFERASE 1.		
Os	Oryza sativa (Rice).		
Oc	Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;		
Oc	Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartioideae; Oryzeae;		
Ox	Oryza.		
Rn	NCBI_TaxID=4530;		
Rf	[1]		
Rp	SEQUENCE FROM N.A.		
Rc	STRAIN-CV, NIPONBARE;		
Ra	Sasaki T., Matsumoto T., Yamamoto K.;		
Rt	"Oryza sativa niponbare (GAJ) genomic DNA, chromosome 6, PAC		
Rt	clone:p0535G04."		
Rl	Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.		
Dr	EMBL; AP000039; BAA3375.1; -		
Dr	InterPro; IPR000051; -		
Dr	InterPro; IPR001189; -		
Dr	Prodont; PD000475; -; 1.		
Kw	Transferase		
Sq	SEQUENCE 380 AA; 42717 MW; B857E3153279CAOF CRC64;		
Query Match 14.3%; Score 452.5; DB 10; Length 380; Best Local Similarity 33.2%; Pred. No. 1.1e-27; Matches 118; Conservative 66; Mismatches 126; Indels 45; Gaps 10.			
Qy	143	ESSAVGYGFQFYGLSQQQNMMDYVRTGTYYORAILQNHTDFKDXIVLDVGGSGTLSTFF	202
Dd	25	KEVDANFYCTYSYLHYOKEMLCEDVRMDAYSASFVRNHNHRGRKVLVDVGTSGSLAIIM	84
Qy	203	AAQGARKIYVEASTMQHAHEVLVKSNNLDRIVYIGKVGEVSLSPROVDIIISEPKMY	262
Dd	85	SAQAARRVYVEATNMAEHARELARADVADIVEYIGSMEDVLPKRVDIYISEMKGX	144
Qy	263	MLFNRMLESYLIAHK-KYIKPSGNFPITGDVHLAPFT-----DEOLYM	305
Dd	145	FLLRESMDSDYICARDRWLKPDGVMPYRHHARMWLPIPSDLAEKNMEDLETMHDMNLFFV	204
Qy	306	EOFTKANRFYOPSFHFVDLSALR--GAAYDEFROPVV--DTFDIRILMAKSVKYTYNF	360
Dd	205	ED-----TESYGVAMNVLTKAUYRAHEKEYULSKAIMWNLHPNOYIGQAAYIKEIDC	256
Qy	361	LEAKGIDLH---RIEIFPKFMHLSGLVHGIAEFDAFGS-----IMTWLSTAP-T	410
Dd	257	LTAETDELREYRAQYTMPIKIDMTF--LAALAGMFVHFGRSGKONPATOEVELSTADPV	313
Qy	411	EPLTFHWYVRCLEFGSPFLFAKAGDTLSGTCILLANK--ROSYSISTIAVOYDOTGSK	463
Dd	314	NGGTHWGQOVFLTPPLKLVNBSGDNYKVSFTYVRSKENHRLMDMETTYELHSSGK	368
RESULT 14			
ID	Q9UZX0	PRELIMINARY;	PRT; 348 AA.
Kc	Q9UZX0;		

DT 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
 DE Y11367B.17 PROTEIN.
 GN Y11367B.17.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
 OC Rhabditidae; Peloderinae; Caenorhabditis.
 OX NCBI_TaxID=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Lennard N.;
 RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=9069613; PubMed=9851916;
 RA none;
 RT "Genome sequence of the nematode C. elegans: A platform for
 RT investigating biology."
 RL Science 282:2012-2018(1998).
 DR EMBL; AL10477; CAB54335.1;
 DR InterPro: IPR000051;
 DR InterPro: IPR001023;
 DR PROSITE: PS00329; HSP70_2; UNKNOWN_1;
 SQ SEQUENCE 348 AA; 39771 MW; 4658749A0EE39725 CRC64;

Query Match 14.2%; Score 449.5; DB 5; Length 348;
 Best Local Similarity 32.9%; Pred. No. 1.6e-27;
 Matches 115; Conservative 62; Mismatches 144; Indels 29; Gaps 8;

QY 125 LKTCRGHTLRSVSEETEE--SSAVQYFQFYGLSOOONMMDYVETGTORAILQNHNTD 183
 Db 1 MSTENGRSADAPVAPAAKELTSDYFDSYAHGCIHEEMKDEKRTTYNSIYHNSHL 60
 QY 184 FRKRIYLVDCGSGILSFPAQAQARKITYAEASTMAQHAELVYKSNLTDRIYVIGKV 243
 Db 61 FRKRVNDVSGTGLISFPAQAKAKRYFAMFESNMALTSKRIITADNNLHIVIAQKV 120
 QY 244 EEV-SLP---EQVDIISPMGYMLFNERMLESTYLAH-KYIKSGNMPTIGDVHLAPF 298
 Db 121 EDVHELPGGLEKDYIISPMGYMLFNERMLESTYLAH-KYIKSGNMPTIGDVHLAPF 180
 QY 299 TDSQQLMEQFTKANFRYQSPFHGVDSALGAAVDEYFROPVDTFDIRILMAKSVYTV 358
 Db 181 ED-----ROYKEDKIHMDSDVYGFNMSAKIKVAL-----KPLVDIVD-----NAQVNT 224
 QY 359 NFEAKEGDHRLEI-----PKFHMHSGLVHGLAFNFDVAFGISIMTWLSTAPTE 411
 Db 225 NNCGLDADLVYKIEDLFFKSDFKLCTRSDDYIQAFVTFEYFESKCHKKTGSPDPV 284
 QY 412 PLTHMYQVRCLEFOSPLFAKADPLSGTCLLIANKROSYSIYAQVDTG 461
 Db 285 QYTHMKQYFYLLKDALTVKKEGELTGSFEMAPKNNERDIDINISFPFGK 334

RESULT 15
 09LJ29 PRELIMINARY; PRT; 399 AA.
 AC 09LJ29
 DT 01-OCT-2000 (TREMBlrel. 15, Created)
 DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
 DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
 DE PROTEIN ARGININE N-METHYLTRANSFERASE-LIKE PROTEIN.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
 OC Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
 OC Brassicales; Brassicaceae; Arabidopsis.
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=COLUMBIA;
 RA Kaneko T., Kato T., Sato S., Nakamura Y., Asamizu E., Tabata S.;

RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=COLUMBIA;
 RX PubMed=10907853;
 RA Nakamura Y.;
 RT "Structural analysis of Arabidopsis thaliana chromosome 3. II.
 RT Sequence features of the regions of 4,251,695 bp covered by ninety p1,
 RT TAC and BAC clones."
 RL DNA Res. 7:217-221(2000).
 DR EMBL; AP000383; BAB01859.1;
 DR InterPro: IPR000051;
 DR InterPro: IPR001312;
 DR ProDom: PD001109;
 KW Transferase; Methyltransferase.
 SQ SEQUENCE 399 AA; 43983 MW; 0C49FOA691529F1A CRC64;

Query Match 14.0%; Score 443; DB 10; Length 399;
 Best Local Similarity 31.7%; Pred. No. 6.5e-27;
 Matches 108; Conservative 71; Mismatches 128; Indels 34; Gaps 8;

QY 139 SERTEESSA-----VOYFQFYGLSOOONMMDYVETGTORAILQNHNTDFKDIYVD 191
 Db 65 SLETSSESPPCPTDEVDVYFHSYAHVGIHEMKRARTETRYREAIMQSLIEGKVYVD 124
 QY 192 VCGSGILSFPAQAQARKITYAEASTMAQHAELVYKSNLTDRIYVIGKVEEVSLEPQ 251
 Db 125 VCGGTGLISFPAQAQAKRYAVAVDASDIYVQAKYKANGSLDKYIVLHGREVEIDEE 184
 QY 252 VDIISPMGYMLFNERMLESTYLAH-KYIKSGNMPTIGDVHLAPTEDEQVMEQFTK 310
 Db 185 VDVIISPMGYMLFNERMLESTYLAH-KYIKSGNMPTIGDVHLAPTEDEQVMEQFTK 240
 QY 311 ANFRYQSPFHGVDSALGAAVDEYFROPVDTFDIRILMAKSVYTVNFEAKEGDLH 369
 Db 241 -SIDFMRVYVIDMSAMMQLKCAFEESVESISGENVLTPMEVFPLEESGPSAS--- 296
 QY 370 RIEIPFHMHSGLVHGLAFNFDVAFGISIM-----TWLSTAPTEPLTHMYQV 420
 Db 297 ---PARK-NSETSIASGSS---SISPSGEVNOKRRNPSDALVISTGSPSPPTHMQDTI 348
 QY 421 CLFOSPLFAKADPLSGTCLLIANKROSYSIYAQVDTG 461
 Db 349 VYFDPIDVDEQDYIEGSVTLSSQSKENKRFNMIHLEYSAG 389

Search completed: June 20, 2001, 10:00:59
 Job time: 198 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: June 20, 2001, 09:55:06 ; Search time 13.98 Seconds

(without alignments)
876.104 Million cell updates/sec

Title: US-09-464-377-2

Perfect score: 3168
Sequence: 1 MAAAAATVGPAGSAGVAG.....PAISNAPSNIPTNTHYGS 608Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 193259 seqs, 2014635 residues

Total number of hits satisfying chosen parameters: 193259

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summariesDatabase : Issued_Patents_AA:*
1: /cgn2_6/prodata/2/1aa/5A.COMB.pep.*
2: /cgn2_6/prodata/2/1aa/5B.COMB.pep.*
3: /cgn2_6/prodata/2/1aa/6A.COMB.pep.*
4: /cgn2_6/prodata/2/1aa/6B.COMB.pep.*
5: /cgn2_6/prodata/2/1aa/PCTUS.COMB.pep.*
6: /cgn2_6/prodata/2/1aa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2290.5	72.3	447	3	US-09-109-204-3
2	481.5	15.2	343	3	US-09-109-204-32
3	127.5	4.0	276	4	US-08-935-263-16
4	117	3.7	531	2	US-08-923-536A-12
5	114	3.6	1261	4	US-09-208-742-4
6	108	3.4	356	1	US-07-959-941-2
7	108	3.4	356	1	US-08-259-924-2
8	107.5	3.4	1289	1	US-07-876-280-4
9	107.5	3.4	1289	1	US-07-675-772-4
10	107.5	3.4	1289	1	US-08-063-170-4
11	107.5	3.4	1289	1	US-08-158-232-4
12	107.5	3.4	1289	1	US-08-304-626-4
13	107.5	3.4	1289	1	US-08-316-501A-4
14	107.5	3.4	1289	2	US-08-611-928-4
15	107.5	3.4	1289	3	US-09-173-891-4
16	107.5	3.4	1289	4	US-09-076-137-4
17	107.5	3.4	1289	5	PCT-US92-03624-4
18	107.5	3.4	1289	6	5281530-3
19	107.5	3.4	1289	6	5426049-4
20	103.5	3.3	696	3	US-08-906-865-4
21	99	3.1	552	1	US-07-662-223-2
22	98.5	3.1	3665	2	US-08-222-617A-13
23	98.5	3.1	3712	2	US-08-222-617A-4
24	98.5	3.1	3712	2	US-08-222-617A-25
25	96.5	3.0	675	1	US-08-386-495-10
26	96.5	3.0	675	5	PCT-US96-02331-10
27	95	3.0	654	1	US-08-083-590A-16

28	95	3.0	654	2	US-08-346-128-35	Sequence 35, Appl
29	95	3.0	654	3	US-08-532-384-16	Sequence 16, Appl
30	95	3.0	2523	1	US-08-185-432-18	Sequence 18, Appl
31	93.5	3.0	661	1	US-08-525-742-2	Sequence 17, Appl
32	92.5	2.9	666	1	US-08-083-590A-17	Sequence 17, Appl
33	92.5	2.9	666	2	US-08-346-128-36	Sequence 36, Appl
34	92.5	2.9	666	2	US-08-532-384-17	Sequence 17, Appl
35	92.5	2.9	1118	2	US-08-724-354D-2	Sequence 2, Appl
36	92.5	2.9	1118	2	US-09-270-984A-2	Sequence 2, Appl
37	92	2.9	1452	2	US-08-449-644-8	Sequence 8, Appl
38	92	2.9	1452	2	US-08-087-244A-8	Sequence 8, Appl
39	91.5	2.9	436	3	US-09-188-579-112	Sequence 112, App
40	91.5	2.9	436	4	US-09-315-444-112	Sequence 112, App
41	91	2.9	240	1	US-07-965-668A-3	Sequence 3, Appl
42	91	2.9	240	2	US-08-950-433-3	Sequence 3, Appl
43	91	2.9	240	3	US-09-186-287-3	Sequence 3, Appl
44	91	2.9	504	1	US-08-457-274A-25	Sequence 25, Appl
45	91	2.9	504	5	PCT-US95-05758-25	Sequence 25, Appl

ALIGNMENTS

RESULT 1
US-09-109-204-3
Sequence 3, Application US/09109204
Patent No. 6060250
GENERAL INFORMATION:
APPLICANT: Lal, Preeti
APPLICANT: Bandman, Olga
APPLICANT: Hillman, Jennifer L.
APPLICANT: Guegler, Karl J.
APPLICANT: Gorgone, Gina A.
APPLICANT: Corley, Neil C.
APPLICANT: Patterson, Chandra
TITLE OF INVENTION: HUMAN TRANSFERASES
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/109,204
FILING DATE: HERewith
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: -
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Cerrone, Michael C
REGISTRATION NUMBER: 39,132
REFERENCE/DOCKET NUMBER: PE-0546 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
TELEFAX: 650-855-0572
TELEX:
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 447 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: BRAITUT21
CLONE: 2525071

US-09-109-204-3

Query Match 72.3%; Score 2290.5; DB 3; Length 447;
Best Local Similarity 98.7%; Pred. No. 4.9e-205;
Matches 441; Conservative 3; Mismatches 2; Indels 1; Gaps 1;

QY 163 MMODVYRTGYQRAIQNTDFKDKIVLDVGGSSGILSFFAAOAGAKKIYAVASTMAOH 222
DB 1 MMODVYRTGYQRAIQNTDFKDKIVLDVGGSSGILSFFAAOAGAKKIYAVASTMAOH 60
QY 223 AEVLVKSNNLTORIVYIPKGVVEVSLPEQVDITISPEMGMLFENRMLSEYLAHKKYLR 282
DB 61 AEVLVKSNNLTORIVYIPKGVVEVSLPEQVDITISPEMGMLFENRMLSEYLAHKKYLR 120
QY 283 SGNMFTTIDVHLAPFTDQLYMEQFTKANFRYQPSFGVDSLALGAAVDEYFROPVVD 342
DB 121 SGNMFTTIDVHLAPFTDQLYMEQFTKANFRYQPSFGVDSLALGAAVDEYFROPVVD 180
QY 343 TFDIRLMAKSKYKYVNFLEAKEGDLHRIEIPKFMHLSGLVHGLAFWEDVAFISIMT 402
DB 181 TFDIRLMAKSKYKYVNFLEAKEGDLHRIEIPKFMHLSGLVHGLAFWEDVAFISIMT 240
QY 403 VMLSTAPTEPLTHWYQVCLFOSPLFAKAGDTLSGTCLLIANKROSYDITVAQVOTGS 462
DB 241 VMLSTAPTEPLTHWYQVCLFOSPLFAKAGDTLSGTCLLIANKROSYDITVAQVOTGS 300
QY 463 KSNLLDLNPFRTYGTTPSPGSHYTPSENMMNTGSTYNLSSGVAVAGMPTAYDLS 522
DB 301 KSNLLDLNPFRTYGTTPSPGSHYTPSENMMNTGSTYNLSSGVAVAGMPTAYDLS 360
QY 523 SYIAGSSVGHNNLPLANTGIYNHSHRSGSTMSTGIYOGSSGAGC-GGGSSSAHAYN 561
DB 361 SYIAGSSVGHNNLPLANTGIYNHSHRSGSTMSTGIYOGSSGAGGSGSTSAHAYN 420
QY 582 NOFTMGPAISMASPMISPTNTMHYGS 608
DB 421 NOFTMGPAISMASPMISPTNTMHYGS 447

RESULT 2

US-09-109-204-32
Sequence 32, Application US/09109204
Patent No. 6060250

GENERAL INFORMATION:

APPLICANT: Lal, Preeti
APPLICANT: Bandman, Olga
APPLICANT: Hillman, Jennifer L.
APPLICANT: Guegler, Karl J.
APPLICANT: Gorgone, Gina A.
APPLICANT: Corley, Neil C.
APPLICANT: Patterson, Chandra
TITLE OF INVENTION: HUMAN TRANSFERASES
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA

ZIP: 94304

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: Windows

SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/109,204

FILING DATE: HERewith

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Cerrone, Michael C.

REGISTRATION NUMBER: 39,132

REFERENCE/DOCKET NUMBER: PF-0546 US

TELECOMMUNICATION INFORMATION:

TELEPHONE: 650-855-0555

TELEFAX: 650-855-0572

TELEX:

INFORMATION FOR SEQ ID NO: 32:

SEQUENCE CHARACTERISTICS:

LENGTH: 343 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

IMMEDIATE SOURCE:

LIBRARY: GenBank

CLONE: GI 1808648

US-09-109-204-32

Query Match 15.2%; Score 481.5; DB 3; Length 343;
Best Local Similarity 33.4%; Pred. No. 1.2e-36;
Matches 113; Conservative 65; Mismatches 129; Indels 31; Gaps 7;

QY 139 SEETESSAVQ-----YFQFYGLSQOMMODVYRTGYQRAIQNTDFKDKIVLDV 192
DB 8 AESSEKPAEDMTSKDYFDSYAFHGIHEMLKDEVRTLLYRNSMFHRLFKRVVLDV 67
QY 193 GCGSGILSFFAAOAGAKKIYAVEASTMAOHAELVKSNNLTORIVYIPKGVVEVSLP-EQ 251
DB 68 GCGSGILSFFAAOAGAKKIYAVEASTMAOHAELVKSNNLTORIVYIPKGVVEVSLP-EQ 127
QY 252 VDIITSEPMGYMLFENRMLSEYLAH-KYKPSGNMFTTIDVHLAPFTDQLYMEQFTK 310
DB 128 VDIITSEPMGYMLFENRMLSEYLAH-KYKPSGNMFTTIDVHLAPFTDQLYMEQFTK 182
QY 311 ANFRYQPSFGVDSLALGAAVDEYFROPVYDFDIRLMAKSKYKYVNFLEAKEGDLH 370
DB 183 YKIHMMENVYGFDMSCCKDAI-----KEPLVDVYDPKQV-----TNCLILEVDIYT 231
QY 371 IEI-----PKFMHLSGLVHGLAFWEDVAFISIMTVMVLSAPTEPLTHWYQVCLF 423
DB 232 VKVEDLFTSPCLQVNRNDYVHLAVFNIEFRCHKRGTGFSPESPYTHMKQTVAYM 291
QY 424 QSPLEAKGDTLSGTCLLIANKROSYDITVAQVOTGS 461
DB 292 EDYLVTKGEEIFGTIGMRPNKNNRDLDTIDDFKG 329

RESULT 3

US-08-935-263-16
Sequence 16, Application US/08935263A
Patent No. 6117669

GENERAL INFORMATION:

APPLICANT: Furuchi, Yasuhiro

APPLICANT: Hoshino, Tatsuo

APPLICANT: Kimura, Hitoshi

APPLICANT: Kiyasu, Tatsuya

APPLICANT: Nagahashi, Yoshie

TITLE OF INVENTION: BIOTIN BIOSYNTHETIC GENES

FILE REFERENCE: Biotin Genes

CURRENT APPLICATION NUMBER: US/08/935,263A

CURRENT FILING DATE: 1997-09-22

EARLIER APPLICATION NUMBER: EP 96115540.5

NUMBER OF FILING DATE: 1996-09-27

NUMBER OF SEQ ID NOS: 23

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 16

LENGTH: 276

TYPE: PRT

ORGANISM: Kurthia sp.

US-08-935-263-16

Query Match 4.0%; Score 127.5; DB 4; Length 276;
Best Local Similarity 20.0%; Pred. No. 0.00084;
Matches 59; Conservative 52; Mismatches 87; Indels 97; Gaps 12;

QY 133 LERSFERSESSAVQYFOFYGLISQOONMODVFRGTGORALIONHTPEKDI-VLD 191

DB 2 IDKOLSKRSEHAKT-----YDAVAVOKNAKOLVD-----LTFQKNSKORINILE 49

QY 192 VGGGSLSEFPAOAGARKIYAVEASTMAQHAENVLSNNLDRIVVPGKVEEVSLEPQ 251

DB 50 ICGGTGLTRLVMTFPPNA-SITAVDLAPGMVEVAKGITMEDRTFICADIEETLWEN 107

QY 252 VDIITSE-----PQGYMLFN-----EMLSEYLHAKKYLKPS 283

DB 108 YDLIISNATFQWLNLPGLTIEQLFTRLTPEGNLIFSTFGIKTFQELHMSYEHAKELQLS 167

QY 284 -----GNMFTIGDV-----HLAPFTD-----EOLYMEQ----- 308

DB 168 IDSSPGQLFALBELSOICEBAIPFSSAFLPTEIKTELELEYQTVREFFTSIKKIGAA 227

QY 309 --TRANRPOPSFHGVDSLALRGAAVDEYFRQPVDFEDIRILMAKSVKYTVNFI 361

DB 228 NSNKNENCORPSF-----FRF-LINITYETKODESGVKATYHCL 265

RESULT 4

US-08-923-536A-12

Sequence 12, Application US/08923536A

Patent No. 5965426

GENERAL INFORMATION:

APPLICANT: SAKAI, Yasuyoshi

APPLICANT: KATO, No. 5965426uo

APPLICANT: SHIBANO, Yuji

TITLE OF INVENTION: PROTEIN DISULFIDE ISOMERASE GENE DERIVED

TITLE OF INVENTION: FROM STRAIN OF METHYLOTROPIC YEAST

NUMBER OF SEQUENCES: 12

CORRESPONDENCE ADDRESS:

ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS, L.L.P.

STREET: 1737 King Street, Suite 500

City: Alexandria

STATE: Virginia

COUNTRY: United States

ZIP: 22314-2756

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: IBM PC compatible

SOFTWARE: Patent Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/923,536A

FILING DATE: 04-SEP-1997

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: JP 8-234287

FILING DATE: 04-SEP-1996

ATTORNEY/AGENT INFORMATION:

NAME: Meuth, Donna M.

REGISTRATION NUMBER: 36,607

REFERENCE/DOCKET NUMBER: 001560-317

TELECOMMUNICATION INFORMATION:

TELEPHONE: (703) 836-6620

TELEFAX: (703) 836-2021

INFORMATION FOR SEQ ID NO: 12:

SEQUENCE CHARACTERISTICS:

LENGTH: 531 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-923-536A-12

Best Local Similarity 21.2%; Pred. No. 0.023;
Matches 81; Conservative 49; Mismatches 130; Indels 122; Gaps 17;

QY 63 AGPDAGIAL-----YSHEDVCYK-----CSVSRETECSRVRGQ-----SFLITLG 104

DB 28 ASPDAVAVKLTADSPESFKNRPVLAEFFAPWCG-----HCKRLGPEFOVADKLYERD 82

QY 105 CNSVLIOGATIPDFCSFPII-----LKTGRHTLERSVSEKTEESSAVQYFOFYGLQ 159

DB 83 IRLAIDTTEEDKLCSSVGIKGYPTLKVFRGYENEPSDAGORTSDSIISYM----- 134

QY 160 QONMODVFRGTGORALIONHTPEKDI-----VLDVGGCS-----GLISFPAQA 206

DB 135 -----VKOSTPPVSTVDDLSIEDTKESENDFYIOVLPRGKSVAGASTFELIAN 186

QY 207 GARKIYAEASTMAQHAENVLSNNLDRIVVPGKVEEVSLEPQYDIITSEPMYMLF- 265

DB 167 GLRDNYSFISTSTSEFSSKYLKG-----IKKSDTPSYILFR 222

QY 266 -NEMLESTLHAKKYLKPSGNFPITIGVHLAPFTDEQLYMEQFTKANFRYQPSFHGVDL 324

DB 223 PHEELSDASISY-----KFDEIDHTLIEF-----LVNESKPLFEGEMDG 260

QY 325 SALRG-----AAVDYFRQPVVD-----TPDIRILMAKSVKYTVNF--LEAKEGDLH----- 369

DB 261 SSFQSYMEKMLPVAIFYFNEISEKDAVSDAISKLAKTHRGKVNFGDLSKYGDLHAKNIN 320

QY 370 -RIEIP-FKFMHLHSGLVHGLA 389

DB 321 MKEEPLRAIHDLATELKYGIS 342

RESULT 5

US-09-208-742-4

Sequence 4, Application US/09208742

Patent No. 6174679

GENERAL INFORMATION:

APPLICANT: Kaufmann, Joerg

TITLE OF INVENTION: C1F150/hnF1150 is Necessary for Cell

TITLE OF INVENTION: Cycle Progression

FILE REFERENCE: 1453.002

CURRENT APPLICATION NUMBER: US/09/208,742

CURRENT FILING DATE: 1998-12-10

NUMBER OF SEQ ID NOS: 6

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 4

LENGTH: 1261

TYPE: PRT

ORGANISM: human

US-09-208-742-4

Query Match 3.6%; Score 114; DB 4; Length 1261;

Best Local Similarity 21.9%; Pred. No. 0.18;
Matches 91; Conservative 64; Mismatches 167; Indels 94; Gaps 20;

QY 216 ASTMAQHAENVLSNNLDRIVVPGKVEEVS--LPEQYDIITSEPMGYLFFNEMLESY 273

DB 483 SATFFKKTIEKLAR-DILIDPIRYOGDIEANEDVQIYEILHSGPSKMMWTLRRLVE-- 539

QY 274 LHAKKYLKPSGNMFPITIGVHLAPFTDEQLYMEQFTKANFRYQPSFHGVDLSALRGAAVD 333

DB 540 -----FTSSGCVL--FVTKKANAEELAN-MIKOE-----GHNGLGLHG-DMD 578

QY 334 EYFRQPVVDTF--DIRILMA-----KSVKYTVNPLEAKEGDLHRIEIPFKHML 380

DB 579 QSERKNKVISDEKFKDIPVLVATDVAAKGLDIPSIKTVINVDVARDIDTHHRIGRTGRAG 638

QY 381 HSGLVHGLAFMFDVAFIGSIM--TWLSTAPTEPLTHWYQVRCLOFQSPPLFAKAGDPLSGT 438

DB 639 EKGVAVTLLTPKDSNFAAGLVNIBGANOHVSKELLDLAMQNMWFKRSR--KGG---KKG 634

QY 439 CLLIA-----NKRQSTDISIVAOVDOTGSKSSNLDLKNPF-F 475

Query Match 3.7%; Score 117; DB 2; Length 531;

DB 695 KNTGGGGLYRERBOLSENNDRGNNAWSE-----AKRSTGAMGRITMKAPFOS 750
OY 476 RYGTTPSPPSHTYSPSENNMNTGSTYNLSSGVAAGNPATYDLSVYAGSSVGHN- 534
DB 751 QYK-----SHFVAASLSNOKAG-----SSAAGASGWTSGNSINSVPTNSAQOCHNS 796
OY 535 --NLIPLATNTGVNTHSMGMSIMSGIYOGSSGAGCGSSSAHYAVNNQFTMG 588
DB 797 PDSPTSAKGIPIGFGNT--GNISGAPVTPYPSAGAGVNNNTASGN--NSRSTGG 847

RESULT 6

US-07-959-941-2
; Sequence 2, Application US/07959941
; Patent No. 5364781
; GENERAL INFORMATION:
; APPLICANT: HUTCHINSON, Charles R.
; APPLICANT: MADDURI, Krishna M.
; APPLICANT: TORTI, Francesca
; APPLICANT: COLOMBO, Anna L.
; TITLE OF INVENTION: PROCESS FOR PREPARING DAUNORUBICIN
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Nikaïdo, Marmelstein, Murray & Oram
; STREET: 655 Fifteenth Street N.W. Suite 330.
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005-5701
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/959,941
; FILING DATE: 19921009
; CLASSIFICATION: 435
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US 793,873
; FILING DATE: 18-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Chiu, Monica F.
; REGISTRATION NUMBER: P-36,105
; REFERENCE/DOCKET NUMBER: 1615-1816CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)638-5000
; TELEFAX: (202)638-4810
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 356 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-07-959-941-2

Query Match 3.4%; Score 108; DB 1; Length 356;
Best Local Similarity 27.6%; Pred. No. 0.083;
Matches 53; Conservative 26; Mismatches 67; Indels 46; Gaps 10;

OY 189 VLDVGGGSGILSFPAAGARKIYAVEASTM-----AQHAEVLVKSNNLTDRIVIPGKV 243
DB 183 VLDVGGGKG---GFAA-AIARRAPHSATVLEMAGYDTARSYLKDEGLSDRDVVEGDF 238
OY 244 EEVSLPEVDVITISEPAGYMLFN-----ERMLESYLAHKRYLKPSCNMFPPTIGDVHLP 297
DB 239 FE-PLPRKADAIT--LSFVLLNMPDHDVAVILTRCAEA---LEPGRIIL-----IHERD 286
OY 298 FTDEQLYMEQFTKANFRYQSPFHGV-----DLSALRGAADVDEFQPVVDFTDIRIL 349
DB 287 DLHENSFNEQFTELDRLMVLVFLGALTRREKMDGLAASAGLVVE-----VRQL 335

OY 350 MAKSVKTYVNF 361
DB 336 PSPITIPDLSL 347

RESULT 7

US-08-259-924-2
; Sequence 2, Application US/08259924
; Patent No. 5563064
; GENERAL INFORMATION:
; APPLICANT: HUTCHINSON, Charles R.
; APPLICANT: MADDURI, Krishna M.
; APPLICANT: TORTI, Francesca
; APPLICANT: COLOMBO, Anna L.
; TITLE OF INVENTION: PROCESS FOR PREPARING DAUNORUBICIN
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Nikaïdo, Marmelstein, Murray & Oram
; STREET: 655 Fifteenth Street N.W. Suite 330
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005-5701
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/259,924
; FILING DATE:
; CLASSIFICATION: 435
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US 793,873
; FILING DATE: 18-NOV-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/959,941
; FILING DATE: 09-OCT-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Kilts, Monica C.
; REGISTRATION NUMBER: 36,105
; REFERENCE/DOCKET NUMBER: 1615-4003
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)638-5000
; TELEFAX: (202)638-4810
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 356 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-259-924-2

Query Match 3.4%; Score 108; DB 1; Length 356;
Best Local Similarity 27.6%; Pred. No. 0.083;
Matches 53; Conservative 26; Mismatches 67; Indels 46; Gaps 10;

OY 189 VLDVGGGSGILSFPAAGARKIYAVEASTM-----AQHAEVLVKSNNLTDRIVIPGKV 243
DB 183 VLDVGGGKG---GFAA-AIARRAPHSATVLEMAGYDTARSYLKDEGLSDRDVVEGDF 238
OY 244 EEVSLPEVDVITISEPAGYMLFN-----ERMLESYLAHKRYLKPSCNMFPPTIGDVHLP 297
DB 239 FE-PLPRKADAIT--LSFVLLNMPDHDVAVILTRCAEA---LEPGRIIL-----IHERD 286
OY 298 FTDEQLYMEQFTKANFRYQSPFHGV-----DLSALRGAADVDEFQPVVDFTDIRIL 349
DB 287 DLHENSFNEQFTELDRLMVLVFLGALTRREKMDGLAASAGLVVE-----VRQL 335
OY 350 MAKSVKTYVNF 361


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MOLECULE TYPE: protein
HYPOTHETICAL: YES
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: BACILLUS THURINGIENSIS
STRAIN: PS17
INDIVIDUAL ISOLATE: PS17b
IMMEDIATE SOURCE:
CLONE: E. coli NM522(pMYC1628) NRRL B-18652
US-08-158-232-4

```

```

Query Match          3.4%; Score 107.5; DB 1; Length 1289;
Best Local Similarity 21.9%; Pred. No. 0.76;
Matches 60; Conservative 36; Mismatches 97; Indels 81; Gaps 11;

```

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QY 383 GLVHGLAFMFDA-FIGSIMTVLSTA-----PTE-----PLTH-----WYQVRC----- 421
DB 536 GNVSTMGPFPEKASGYGVKEMLGANAMKLSFGOSIGIPITNTVTSGETQIRCRVANSND 595
QY 422 -----LFQSPLEFAKADTLG-----TCLLIANKROSVDISIAQ-- 456
DB 596 NTNVEFNVDTGGANPIFOQINPASTVDNNTGVGANGVYVKSIAITDNTSFTYKIPAKTI 655
QY 457 -VDQGSKSSNLLDKNPFRYGTTPSPPGSHYTSSEN-----MNNTGSTVNLSS 508
DB 656 NVHLTNGSSDVFLEDRIFEVPLIESNTVTIFNNSYTTGSANLIPALPIMSTSSDKALTG 715
QY 509 GVAVAG-----MPTAYDLSVYAGSSVGHNNLIPLANTGIYNHHSRSGSI 555
DB 716 SMSITGRTPNSDALLRFFKTYNDQTIPIPSGKDFNTLTLEID-----I 762
QY 556 MSTGIQSSGAGGSSSAHYAVNNOFTMGSP 589
DB 763 VSIDIFVG-SGLHSGDSIKLDFTNNSGSGSP 795

```

```

RESULT 12
US-08-304-626-4
; Sequence 4, Application US/08304626
; Patent No. 5616495
; GENERAL INFORMATION:
; APPLICANT: Payne, Jewel M.
; APPLICANT: Kennedy, M. Keith
; APPLICANT: Randall, John Brooks
; APPLICANT: Meier, Henry
; APPLICANT: Uick, Heidi Jane
; APPLICANT: Foncecrada, Luis
; APPLICANT: Schnepf, Harry E.
; APPLICANT: Schwab, George E.
; TITLE OF INVENTION: No. 5616495el Bacillus thuringiensis Isolates
; TITLE OF INVENTION: Active Against Hymenopteran Pests and Genes Encoding
; TITLE OF INVENTION: Hymenopteran Active Toxins
; NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David R. Saliwanchik
; STREET: 2421 N.W. 41st Street, Suite A-1
; CITY: Gainesville
; STATE: FL
; COUNTRY: USA
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/304,626
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/887,980
; FILING DATE:

```

```

ATTORNEY/AGENT INFORMATION:
; NAME: Saliwanchik, David R.
; REGISTRATION NUMBER: 31,794
; REFERENCE/DOCKET NUMBER: M/SCJ 104
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 904-375-8100
; TELEFAX: 904-372-5800
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1289 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: YES
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: BACILLUS THURINGIENSIS
; STRAIN: PS17
; INDIVIDUAL ISOLATE: PS17b
; IMMEDIATE SOURCE:
; CLONE: E. coli NM522(pMYC1628) NRRL B-18652
US-08-304-626-4

```

```

Query Match          3.4%; Score 107.5; DB 1; Length 1289;
Best Local Similarity 21.9%; Pred. No. 0.76;
Matches 60; Conservative 36; Mismatches 97; Indels 81; Gaps 11;

```

```

QY 383 GLVHGLAFMFDA-FIGSIMTVLSTA-----PTE-----PLTH-----WYQVRC----- 421
DB 536 GNVSTMGPFPEKASGYGVKEMLGANAMKLSFGOSIGIPITNTVTSGETQIRCRVANSND 595
QY 422 -----LFQSPLEFAKADTLG-----TCLLIANKROSVDISIAQ-- 456
DB 596 NTNVEFNVDTGGANPIFOQINPASTVDNNTGVGANGVYVKSIAITDNTSFTYKIPAKTI 655
QY 457 -VDQGSKSSNLLDKNPFRYGTTPSPPGSHYTSSEN-----MNNTGSTVNLSS 508
DB 656 NVHLTNGSSDVFLEDRIFEVPLIESNTVTIFNNSYTTGSANLIPALPIMSTSSDKALTG 715
QY 509 GVAVAG-----MPTAYDLSVYAGSSVGHNNLIPLANTGIYNHHSRSGSI 555
DB 716 SMSITGRTPNSDALLRFFKTYNDQTIPIPSGKDFNTLTLEID-----I 762
QY 556 MSTGIQSSGAGGSSSAHYAVNNOFTMGSP 589
DB 763 VSIDIFVG-SGLHSGDSIKLDFTNNSGSGSP 795

```

```

RESULT 13
US-08-316-301A-4
; Sequence 4, Application US/08316301A
; Patent No. 5753492
; GENERAL INFORMATION:
; APPLICANT: Schnepf, Harry E.
; APPLICANT: Schwab, George E.
; APPLICANT: Payne, Jewel M.
; APPLICANT: Narva, Kenneth E.
; APPLICANT: Foncecrada, Luis
; TITLE OF INVENTION: No. 5753492el Nematode-Active Toxins and Genes
; TITLE OF INVENTION: Which Code Therefor
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Saliwanchik & Saliwanchik
; STREET: 2421 N.W. 41st Street, Suite A-1
; CITY: Gainesville
; STATE: FL
; COUNTRY: USA
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; OPERATING SYSTEM: IBM PC compatible
; FILING DATE:

```

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/316, 301A
FILING DATE: 30-SEP-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/871, 510
FILING DATE: 23-APR-1992
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/693, 018
FILING DATE: 03-MAY-1991
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/565, 544
FILING DATE: 10-AUG-1990
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/084, 653
FILING DATE: 12-AUG-1987
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/830, 050
FILING DATE: 31-JAN-1992
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Lloyd, Jeff
REGISTRATION NUMBER: 35, 589
REFERENCE/DOCKET NUMBER: MA20CCCD1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 904-375-8100
TELEFAX: 904-372-5800
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1289 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: BACILLUS THURINGIENSIS
INDIVIDUAL ISOLATE: PS17
IMMEDIATE SOURCE:
CLONE: E. coli NM522(PMYC 1628) NRRL B-18652
US-08-316-301A-4

Query Match 3.4%; Score 107.5; DB 1; Length 1289;
Best Local Similarity 21.9%; Pred. No. 0.76;
Matches 60; Conservative 36; Mismatches 97; Indels 81; Gaps 11;

383 GLVHGLAFWFDVA-FIGSITVWLSFA-----PTE-----PLTH-----WYVRC----- 421
DB 536 GNVSTMGFPPEKASYGTIVKWKLANAKLSFGOSIGDITVTSGETVIGRIRYASND 595
422 -----LPSPLFAKAGDTLSG-----TCLLANKROSYDISVAQ-- 456
DB 596 NTWVFVNDVGGANPIQOINFASTVNNNGVGVGANGVYVYKSIATIDNSTVYIIPAKTI 655
457 -VDQFGSKSSNLLDLKAPFRYGTTPSPPGSHYTSBSEN-----MNWTGSTYVNISS 508
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RESULT 14
US-08-611-928-4
Sequence 4, Application US/08611928
Patent No. 5824792
GENERAL INFORMATION:
APPLICANT: Payne, Jewel
APPLICANT: Kennedy, M. Keith
APPLICANT: Randall, John Brooks
APPLICANT: Meier, Henry
APPLICANT: Uick, Heidi Jane
APPLICANT: Foncerra, Luis
APPLICANT: Schepf, H. Ernest
APPLICANT: Schwab, George E.
APPLICANT: Fu, Jenny
TITLE OF INVENTION: No. 5824792el Bacillus thuringiensis Toxins Active
TITLE OF INVENTION: Against Hymenopteran Pests
NUMBER OF SEQUENCES: 51
CORRESPONDENCE ADDRESS:
ADDRESSEE: David R. Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
STATE: FL
COUNTRY: USA
ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/611, 928
FILING DATE: 06-MAR-1996
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/158, 232
FILING DATE: 24-NOV-1993
APPLICATION NUMBER: US 07/887, 980
FILING DATE: 22-MAY-1992
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/797, 645
FILING DATE: 25-NOV-1991
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/703, 977
FILING DATE: 22-MAY-1991
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Saliwanchik, David R.
REGISTRATION NUMBER: 31,794
REFERENCE/DOCKET NUMBER: M/SCJ104.C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 904-375-8100
TELEFAX: 904-372-5800
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1289 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: BACILLUS THURINGIENSIS
INDIVIDUAL ISOLATE: PS17b
IMMEDIATE SOURCE:
CLONE: E. coli NM522(PMYC1628) NRRL B-18652
US-08-611-928-4

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 20, 2001, 16:46:39 ; Search time 2266.15 seconds
(without alignments)
13031.227 Million cell updates/sec

Title: US-09-464-377-1

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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1022815 segs, 4726426750 residues

Total number of hits satisfying chosen parameters: 20456230

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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174 a	320 c
320 c	347 g
160 t	4 others

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Best Local Similarity	90.0%;	Pred. No. 1.8e-185;		
Matches 788; Conservative	3;	Mismatches 82;	Indels 3;	Gaps 1;

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QY	243	cagccataaagatggtgtgttttcaaatgttcggtgccggaagagaaggtgca	302
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QY	303	tgttggcgagcagcttcctcatcatcaaccttgcctgcgcacagcgcctccatccagttgc	362
Db	430	TGTGGGCAAGCAGTCTCTTATCATATCACCCTGGGCTGCAACAGCGTCTCATCCAGTTGCG	489
QY	363	cacaccccaagatttcgttcttcttaacaatccttgaaaacctgtcgggccacacact	422
Db	490	CACACCCCAAGATTTCTTCTCTCTCTTCTTAAACATCTGTAACATCTGCGGGCCACACCT	549
QY	423	ggagcgctcgtgttctcagtgagcgagcagagaaacctcagctgtgcagtaacctcagtt	482
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QY	723	agacgcgatctgtgtcatccctctgccaagtgtgaggagttccatctgtcctgcgacaagtga	782
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LOCUS	943 bp mRNA
DEFINITION	AL527554 LTI_NF003_NBC3 Homo sapiens cDNA clone CSDDC024YE24 5 prime, mRNA sequence.
ACCESSION	AL527554
VERSION	AL527554.1 GI:12791047
KEYWORDS	EST.
SOURCE	human.
ORGANISM	Homo sapiens
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE	1 (bases 1 to 943)

QY	1410	caagctcaagtaaacctcttgatctaaagaacccctcttcaggtaacacaggtacaaacccc	1469
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Db	604	GAAAGT-GTGAACACCCGGGTCAACAGCCCTTGTGCTATGGGAACCTTGACCATTTGTATC	661
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 Seq primer: 5'-ATTAGGTGACTATAG-3'
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http://www.rzp.de."

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Query Match	19.5%;	Score 610.6;	DB 151;	Length 688;
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2110 cctggttcgtactctccactctgacctggtcttgacatctgctggaagaggaagtcctc 2169

db 76 ccgcttctctgactcttccgacccgcttmgacattctgctggaaggcaagtctc 135

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Q7 2230 ccctgcagcaccacccacaccccgctcctctgcacctccctcactggtgtgcagcac 2289

Db 196 CCTGGCAGCACCACCCACCAACCGTCTTGCACCTCCCTCAACTGGGGTGGCAGCAC 255

QY 2290 agcagctgacctctcttcaactaccaggcacatggtcaccatggcgtagatgct 2349

Db 256 AGCCGGCTNGACCTCTCTTCACTACCGAGCCACATGGTCACCATGGGGCTGACATGCT 315

2350 acatttttttaatttttttaacaaaaaaccaatattcaaacccacagacctctgaag 2409

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D6 436 AGGGTGGCCCTNTCAAGCCTTCAGAGTGGGCACAGCCNCCTCCACCAAGGTTACCC 495

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D6 616 TGTGTACCCCTGGGGCTACTGGGGGAGAGANAGANACCTCAAAGATGTGTACACACACACAGA 675

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 VERSION BG420290.1 GI:13326796
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 REFERENCE 1 (bases 1 to 919)
 NIH-MGC <http://mgi.mc.man.ac.uk/>.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: DCTD/DRP
 cDNA Library Preparation: Ling Hong/Rubin Laboratory
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
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 adaptor: GCCACAG(C). Size-selected >500bp for average
 insert size 1.8kb. Library constructed by Ling Hong in
 the laboratory of Gerald M. Rubin (University of
 California, Berkeley) using ZAP-cDNA synthesis kit
 (Stratagene) and Superscript II RT (Life Technologies)."
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 Db 483 GGGCTGTGCCAGGCG -TGGCTTTTGGTTTACAGTCTTTCATTCGCTCATATATGAC 541
 QY 1231 gtgtgatacccaagcccaacagagagcccttgacccaactgtatccaggtccgtgctc 1290
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 Db 542 GTGTGGCTGTCCAGAGCCCGACAGAGCCCTGACCCACTGTGACAGGTGC -GGTCTG 599
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 Db 600 TTCCAGTCCACACCTGTGCGC -AGGCAAGGGGACACGCTCTCAGGACATGCTTGCTTAT 658
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 LOCUS H3010B08-3 NIA Mouse 15K cDNA clone Set Mus musculus cDNA clone
 DEFINITION H3010B08 3', mRNA sequence.
 ACCESSION BG063675
 VERSION BG063675.1 GI:12546238
 KEYWORDS EST.
 SOURCE house mouse.
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 578)
 Kargul, G.J., Dudekula, D.B., Qian, Y., Lim, M.K., Jaradat, S.A., Tanaka
 'T.S., Carter, M.G. and Ko, M.S.H.
 TITLE Verification and initial annotation of NIA mouse 15K cDNA clone set
 JOURNAL Unpublished (2001)
 COMMENT Other ESTs: H3010B08-5
 Contact: George J. Kargul
 Laboratory of Genetics
 National Institute on Aging/National Institutes of Health
 333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA
 Email: cdna@nigun.grc.nia.nih.gov
 This clone set has been freely distributed to the community. Please
 visit <http://ligun.grc.nia.nih.gov/cDNA/15k.html> for details.
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 Plate: H3010 row: B column: 08
 High quality sequence stop: 578
 POLYA=yes.
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libraries"

/Lab.Host="DH10B"
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Mol Genet 7: 1967-1978."

BASE COUNT 127 a 125 c 178 g 148 t

ORIGIN

Query Match 17.7%; Score 553.-2; DB 173; Length 578;
Best Local Similarity 98.6%; Pred. No. 2.3e+138;

Matches 558; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

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	DEFINITION	mus6d02.r1 Striatagene mouse embryonic carcinoma (#937317)			Mus	
	ACCESSION	AA215095				
	VERSION	AA215095.1	GI:1814823			
	KEYWORDS	EST				
	SOURCE	house mouse.				
	ORGANISM	Mus musculus				
	REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
	AUTHORS	1 (bases 1 to 568)				
		Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubouque, T., Gaisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenger, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Thaising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and Waterston, R.				
	TITLE	The WashU-HHMI Mouse EST Project				
	JOURNAL	Unpublished (1996)				
	COMMENT	Contact: Marra M/Mouse EST Project WashU-HHMI Mouse EST Project Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email: mouseest@wustl.edu This clone is available royalty-free through LNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. MG1:397307 Seq primer: -28ml3 rev1 ET from Amersham High quality sequence stop: 464.				
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GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: June 20, 2001, 18:45:25 ; Search time 89.36 Seconds
(without alignments)
6476.648 Million cell updates/sec

Title: US-09-464-377-1

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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 317530 seqs, 92630169 residues

Total number of hits satisfying chosen parameters: 635060

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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1	1494.2	47.8	2224	3	US-09-109-204-6 Sequence 6, Appl
2	493	15.8	621	3	US-09-109-204-24 Sequence 24, Appl
3	443	14.2	549	3	US-09-109-204-25 Sequence 25, Appl
4	420	13.4	647	3	US-09-109-204-26 Sequence 26, Appl
5	284.2	9.1	631	3	US-09-109-204-23 Sequence 23, Appl
6	222.2	7.1	258	3	US-09-109-204-22 Sequence 22, Appl
7	221.4	7.1	256	3	US-09-109-204-21 Sequence 21, Appl
8	139.8	4.5	529	3	US-09-109-204-28 Sequence 28, Appl
9	107.8	3.5	220	3	US-09-109-204-29 Sequence 29, Appl
10	106.6	3.4	655	3	US-09-109-204-27 Sequence 27, Appl
11	70.2	2.2	579	4	US-08-991-789A-147 Sequence 147, App
12	48.6	1.6	1028	4	US-08-118-200-1 Sequence 1, Appl
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	37	40.2	1.3	6085	4	US-09-029-603-4	Sequence 4, Appl
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	45	39.8	1.3	2140	5	PCT-US95-04203-1	Sequence 1, Appl

ALIGNMENTS

RESULT 1
US-09-109-204-6
Sequence 6, Application US/09109204
Patent No. 6060250
GENERAL INFORMATION:
APPLICANT: Lal, Preeti
APPLICANT: Bandman, Olga
APPLICANT: Hillman, Jennifer L.
APPLICANT: Guegler, Karl J.
APPLICANT: Gorgone, Gina A.
APPLICANT: Corley, Neil C.
APPLICANT: Patterson, Chandra
TITLE OF INVENTION: HUMAN TRANSFERASES
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/109,204
FILING DATE: HERewith
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
ATTORNEY/AGENT INFORMATION:
NAME: Carione, Michael C
REGISTRATION NUMBER: 39,132
REFERENCE/DOCKET NUMBER: PF-0546 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
TELEFAX: 650-855-0572
TELEX:
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 2224 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: BRAITUT21
CLONE: 2525071


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; Patent No. 6060250
; GENERAL INFORMATION:
; APPLICANT: Lal, Preeti
; APPLICANT: Bandman, Olga
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Guegler, Karl J.
; APPLICANT: Gorgone, Gina A.
; APPLICANT: Corley, Neil C.
; APPLICANT: Paterson, Chandra
; TITLE OF INVENTION: HUMAN TRANSFERASES
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/109,204
; FILING DATE: HERewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Ceirone, Michael C
; REGISTRATION NUMBER: 39,132
; REFERENCE/DOCKET NUMBER: PF-0546 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-855-0555
; TELEFAX: 650-855-0572
; TELEX:
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 621 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: N/A
; CLONE: SAEAI0009P1
US-09-109-204-24
Query Match 15.8%; Score 493; DB 3; Length 621;
Best Local Similarity 88.0%; Pred. No. 2,4e-112;
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US-09-109-204-25/C										
Sequence 25, Application US/09109204										
Patent No. 6060250										
GENERAL INFORMATION:										
APPLICANT: Lal, Preeti										
APPLICANT: Bandman, Olga										
APPLICANT: Hillman, Jennifer L.										
APPLICANT: Guegler, Karl J.										
APPLICANT: Gorogone, Gina A.										
APPLICANT: Corley, Neil C.										
APPLICANT: Patterson, Chandra										
TITLE OF INVENTION: HUMAN TRANSFERASES										
NUMBER OF SEQUENCES: 32										
CORRESPONDENCE ADDRESS:										
ADDRESSEE: Incyte Pharmaceuticals, Inc.										
STREET: 3174 Porter Drive										
CITY: Palo Alto										
STATE: CA										
COUNTRY: USA										
ZIP: 94304										
COMPUTER READABLE FORM:										
MEDIUM TYPE: Diskette										
COMPUTER: IBM Compatible										
OPERATING SYSTEM: Windows										
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2										

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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/109,204
FILING DATE: HEREWITH
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Cerione, Michael C
REGISTRATION NUMBER: 39,132
REFERENCE/DOCKET NUMBER: PF-0546 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
TELEFAX: 650-855-0572
TELEX:
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 549 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: N/A
CLONE: SAEA03283F1
US-09-109-204-25

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Query Match          14.2%; Score 443; DB 3; Length 549;
Best Local Similarity 89.4%; Pred. No. 4.6e-100;
Matches 489; Conservative 0; Mismatches 55; Indels 3; Gaps 1;

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QY 1230 cgtgtggtatccacagcccaacagagccctgagcccaatgtgtaccaggttcggtgctt 1289
DB 549 CGGTGGCTGTCACAGCCCGACAGAGCCCTGACCCACTGTGATCAGAGGTGGGCTCT 490
QY 1290 ctccagagtcagctgttttgcagagccgggagcagctctcagggagcagctgtctat 1349
DB 489 GTTCAGTCACTGTTGCTCCCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 430
QY 1350 tgcacacaaagacagagctatgacatcagttatgttgcagaggtgagcagagctc 1409
DB 429 TGCCACAAAGACAGAGTACGACATCATGATTTGTCAGGAGTGGACAGACGGGCTC 370
QY 1410 caagtcagtaacctgtgatactaaagaccccttcaggtacagagttacaacccc 1469
DB 369 CAGGTCCAGTACCTCTGTGATCTGAAAAACCCCTCTTATGATACAGGAGCAGACGCC 310
QY 1470 ataccacccacccctgagctacacacacacacacacacacacacacacacacacac 1529
DB 309 CTCACCCCAACCCGGCTCCCACTACATCTCTCTCGAAAAACATGTGAAACAGGCGCAG 250
QY 1530 caactaatactcagcagcgaggtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1589
DB 249 CACCTAACACCTCAGACGCGGAGTGGCGGAGTGGCGGAGTGGCGGAGTGGCGGAGTGG 190
QY 1590 cagttgtattgcccggcggtccaggtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1649
DB 189 CAGTGTATTGCGAGTGTGCTCAGCGGCGGCGCACAAACACTGTTCTTTAGCAACAC 130
QY 1650 agggattgtcaatcaacacacacacacacacacacacacacacacacacacacacac 1709
DB 129 GGGGATTGTCAATCAACACCACTCCCGATGGCTCCATATATGACACGGGAGTTGTCCA 70
QY 1710 aggtctcctcaggtgtccagag--gagcggtgtgtgtgtgtgtgtgtgtgtgtgtgt 1766
DB 69 AGGGTCTCTCGGGGCGGAGGAGGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 10
QY 1767 caaccag 1773
DB 9 CAGCGCAG 3
RESULT 4

```

```

US-09-109-204-26
Sequence 26, Application US/09109204
Patent No. 6060250
GENERAL INFORMATION:
APPLICANT: Lal, Preeti
APPLICANT: Bandman, Olga
APPLICANT: Hillman, Jennifer L.
APPLICANT: Guegler, Karl J.
APPLICANT: Gorgone, Gina A.
APPLICANT: Corley, Neil C.
APPLICANT: Patterson, Chandra
TITLE OF INVENTION: HUMAN TRANSFERASES
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/109,204
FILING DATE: HEREWITH
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Cerione, Michael C
REGISTRATION NUMBER: 39,132
REFERENCE/DOCKET NUMBER: PF-0546 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
TELEFAX: 650-855-0572
TELEX:
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 647 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: N/A
CLONE: SAEA01931R1
US-09-109-204-26
Query Match          13.4%; Score 420; DB 3; Length 647;
Best Local Similarity 83.5%; Pred. No. 2.2e-94;
Matches 541; Conservative 0; Mismatches 87; Indels 20; Gaps 5;

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QY 1392 ggttgaccagacaggtcccaagtcagtaacctgtgtgtgtgtgtgtgtgtgtgtgt 1451
DB 1 GGTGAGCAGACGCGGCTCCCAAGTCACTGATCTGAAAAACCCCTTTTATG 60
QY 1452 gtacacaggtacacacacacacacacacacacacacacacacacacacacacacac 1511
DB 61 ATACAGGGGCAACAGCCCTCACCCCAACCCGCTCCCACTACATCTCTCGAAAA 120
QY 1512 tatgtgaacacaggaagacactaatactcagcagcggtgtgtgtgtgtgtgtgtgtgt 1571
DB 121 CATGTGAGACAGGCGGAGCAGACTCAACCTCAGACGCGGAGTGGCGGAGGATGCC 180
QY 1572 taagtctcagacacagcaggtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1631
DB 181 GACCGCTATGACTTGTGAGCACTGTATTGCGCAGTGGCTCCAGCGGCGGCGCACAAAC 240
QY 1632 gattccctgtacacacaggtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1691

```


FILED DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Cerione, Michael C
REGISTRATION NUMBER: 39,132
REFERENCE/DOCKET NUMBER: PF-0546 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
TELEFAX: 650-855-0572
TELEX:
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 258 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: BLADTUT07
CLONE: 1889292H1
US-09-109-204-22

Query Match 7.1%; Score 222.2; DB 3; Length 258;
Best Local Similarity 92.5%; Pred. No. 7.7e-46;
Matches 233; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

QY 290 cagagtcagtcgtgtgagcagacagtccttcacacccctggctgacagcgtcc 349
DB 1 CAGAGTCAGCCCTGGGCGAGCAGTCCTTCATCACCCTGGGCTGCACAGCGCTCC 60
QY 350 tcatcagtttgcagacccacagatttcgtcttcttcaaacatcctaaacgttc 409
DB 61 TCATCAGTTGCGCACACCCAGATTTCGTCTTCAACATCCTAAACCTGCC 120
QY 410 gggagccacactgagcgcctctgttccagtcagcagagaagaaatccctcagctg 469
DB 121 GGGGCGCACACCTGGAGCGGTCTGTTCAGCAGCGAGGAGATCTTTCGCGCTGC 180
QY 470 agtaactcagttctatgtgtacctatccacagacagaaatgagcagactatgtgc 529
DB 181 AGTAACCTCCAGTTTATGGCTACCTGTCCAGCAGCAGAAATGATCAGAGACTACGTC 240
QY 530 ggaacagcact 541
DB 241 GGACAGCACT 252

RESULT 7
US-09-109-204-21
Sequence 21, Application US/09109204
Patent No. 6060250

GENERAL INFORMATION:
APPLICANT: Lal, Preeti
APPLICANT: Bandman, Olga
APPLICANT: Hillman, Jennifer L.
APPLICANT: Guegler, Karl J.
APPLICANT: Corley, Neil C.
APPLICANT: Gorgone, Gina A.
TITLE OF INVENTION: HUMAN TRANSFERASES
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/109,204
FILING DATE: HEREWITH
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Cerione, Michael C
REGISTRATION NUMBER: 39,132
REFERENCE/DOCKET NUMBER: PF-0546 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
TELEFAX: 650-855-0572
TELEX:
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 256 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: BRAITUT21
CLONE: 2525071H1
US-09-109-204-21

Query Match 7.1%; Score 221.4; DB 3; Length 256;
Best Local Similarity 91.8%; Pred. No. 1.2e-45;
Matches 234; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

QY 385 ttctacaacatccctgaaacactgctcgagggccacacacacgagcgtctgttccagtcag 444
DB 2 TTCTACAACATCCGAAACCTGCGGGGCCACACCTGGAGCGGTCTGTTCAGCGAG 61
QY 445 cggacagaggaatccctagctgtgtcagtaacttcagttctatgtgtacctatccacag 504
DB 62 CGGACGAGAGAGTCTTCTGCCGTGCACTTCCAGTTTATGGCTACTCTCCACGAG 121
QY 505 cagacatgatgacagactatgtgcgagcagacactacacagcgtgcgactcagagac 564
DB 122 CAGAACATGATGACGAGACTAGTCGAGCAGACACTACCAAGCGCCATCCTGCAAAAC 181
QY 565 caccagacttcagagcaaatcgtctatagatgtgagcgttcgagacactgtgca 624
DB 182 CACACCGACTTCAAGAGACATGTTCTTGATGTGGCTGTGGCTGTGGATCTGTGC 241
QY 625 ttlttgctgtcaaa 639
DB 242 TTTTTCGCCGCCAA 256

RESULT 8
US-09-109-204-28
Sequence 28, Application US/09109204
Patent No. 6060250

GENERAL INFORMATION:
APPLICANT: Lal, Preeti
APPLICANT: Bandman, Olga
APPLICANT: Hillman, Jennifer L.
APPLICANT: Guegler, Karl J.
APPLICANT: Corley, Neil C.
APPLICANT: Gorgone, Gina A.
TITLE OF INVENTION: HUMAN TRANSFERASES
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:

MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: Windows
 SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/109,204
 FILING DATE: HEREMITH
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER:
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Cerrone, Michael C
 REGISTRATION NUMBER: 39,132
 REFERENCE/DOCKET NUMBER: PF-0546 US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 650-855-0555
 TELEFAX: 650-855-0572
 TELEX:
 INFORMATION FOR SEQ ID NO: 28:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 529 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 IMMEDIATE SOURCE:
 LIBRARY: BRSTNOT09
 CLONE: 1664573F6
 US-09-109-204-28

Query Match	4.5%	Score 139.8;	DB 3;	Length 529;
Best Local Similarity	77.0%	Pred. No. 1.9e+25;		
Matches 218; Conservative	0;	Mismatches 35;	Indels 10;	Gaps 4

OY	2295	gctgagacccctccctcaacacacagcgacacatggtacatggtgagctgagcctgctt	2355
Db	34	GCGGGGCCTCCCTTCGACGACCAAGGCTTC--GGTCACAAGGACCTGACATGCTGCTTT	91
OY	2355	tttbaatttattttttttaaagaaagaacagtggttaacccaagaacctctgtagaacac	2415
Db	92	TTTTTAATTTATTTTTTATGAAAGAAACACAGTGTCAATCCGACACCTCTGTGAAGC	151
OY	2415	cggcttgg--cggcgcaagacgacgacggccctgttctctatgcccagagag--ttctagtgtgaag	2475
Db	152	AGGCGGGCGCGGCGGAGCCAGCAGCGCCCTCTCCCTTAAGACTCAGAGGCGCGCGGGGAGAGG	211
OY	2473	gtggccctgtgcaagcctctcagagtgggacagccctccccaacaaaggtttcaactcaa	2533
Db	212	GTNNCCCCCGGAGGGCTTCAGGG-----NNNNCCCTCCCAACCAAGGGTCACTTCACA	265
OY	2533	cttgaatgtatacaaaccaaccagctgttccaaagagcctagtccct	2575
Db	266	CTTGAATGTATACANCCCANCCCACTGTCTGGAGAGGCTCCGCTCTT	308

RESULT 9
 US-09-109-204-29
 : Sequence 29, Application US/09109204
 : Patent No. 6060250
 :
 : GENERAL INFORMATION:
 :
 : APPLICANT: Lal, Preeti
 : APPLICANT: Bandman, Olga
 : APPLICANT: Hillman, Jennifer L.
 : APPLICANT: Guegler, Karl J.
 : APPLICANT: Gorgone, Gina A.
 : APPLICANT: Corley, Neil C.
 : APPLICANT: Paterison, Chandra
 : TITLE OF INVENTION: HUMAN TRANSFERASES
 : NUMBER OF SEQUENCES: 32
 :
 : CORRESPONDENCE ADDRESS:
 :
 : ADDRESSEE: Incyte Pharmaceuticals, Inc
 : STREET: 3174 Porter Drive

CITY: Palo Alto
 STATE: CA
 COUNTRY: USA
 ZIP: 94304
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: Windows
 SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/109,204
 FILING DATE: HERewith
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER:
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Cerrone, Michael C
 REGISTRATION NUMBER: 39,132
 REFERENCE/DOCKET NUMBER: PP-0546 US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 650-855-0555
 TELEFAX: 650-855-0572
 TELEX:
 INFORMATION FOR SEQ ID NO: 29:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 220 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 IMMEDIATE SOURCE:
 LIBRARY: LUNCTUT03
 CLONE: 1474156T1
 US-09-109-204-29

Query Match	3.54	Score	107.8	DB	3	Length	220
Best Local Similarity	78.9%	Pred. No.	1e-17				
Matches	168	Conservative	0	Mismatches	37	Indels	8
						Gaps	3

QY	2357	tttaatttatttllttttacgaaagaacccggtgtcaaccacagaccctctyagaacccg	2416
Db	6	TTAATTTATTTTATGAAAAAGAACCGTGTCAATCCGAGACCCCTGTGAAGCCAG	65
QY	2417	gcctcg -cgcccaagccagcagccctctgtctctaaagccaaag -tttagttagaggt	2474
Db	66	GCGCGCCGGGCCAGCCAGCAGCCCTCTTCCTTAAGCTCAGAGGCGCGCGGGAGGGGT	125
QY	2475	ggccctgtcaagccttcagagtgtgacacagccctccaccacaaaggttcaaccttaact	2534
Db	126	GGCCCGCGCCAGGCTTCAGAGG-----GCCCCCTCCCCACCAAAGGTTCACTCACACT	179
QY	2535	tgaatgtacaacacccagcgtgtccaagaagcc	2567
Db	180	TGAATGTACAACCCACCCCACTGTGGGGAAGCC	212

RESULT 10
US-09-109-204-27
Sequence 27, Application US/09109204
Patent No. 6060250
GENERAL INFORMATION:
APPLICANT: Lal, Preeti
APPLICANT: Bandman, Olga
APPLICANT: Hillman, Jennifer L.
APPLICANT: Guejler, Karl J.
APPLICANT: Gorgone, Gina A.
APPLICANT: Corley, Neil C.
APPLICANT: Patterson, Chandra
TITLE OF INVENTION: HUMAN TRANSFERASES
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 20, 2001, 16:51:39 ; Search time 4073.48 Seconds
(without alignments)
11862.400 Million cell updates/sec

Title: US-09-464-377-1

Sequence: 1 agggggcctggagccgacc.....taaaagtgttcttctgtaa 3124

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1344157 seqs, 7733874588 residues

Total number of hits satisfying chosen parameters: 2688314

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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97: gb_pl13:*
98: em_ba3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	2256.4	72.2	2336	94	BC003964 Mus muscu
3	1355.4	43.4	233830	75	AC073731 Mus muscu
4	1141.2	36.5	2160	88	AF055027 Homo sapi
5	745.8	23.9	1917	94	BC003289 Mus muscu
6	745.8	23.9	2107	94	BC002282 Mus muscu
7	409.2	13.1	500	10	AX079470 Sequence
8	408	13.1	11218	63	AC013033 Drosophila

AC009189 Drosophila
AC009365 Drosophila
AC079434 Sequence
AC011445 Homo sapiens
AC007542 Homo sapiens
AC007371 Mus musculus
AF063559 Homo sapiens
BC002729 Homo sapiens
AL001441 Homo sapiens
AL055559 Homo sapiens
AC074376 Homo sapiens
U06882 Rattus norvegicus
AF166520 Mus musculus
BC002249 Mus musculus
AF032177 Mus musculus
AF032716 Mus musculus
U08213 Human protein
BC000727 Homo sapiens
AX017209 Sequence
X93220 H. sapiens
Y10807 H. sapiens
Y10806 H. sapiens
Y10805 H. sapiens
D65604 Homo sapiens
AF059530 Rattus norvegicus
Continuation (9 of 10)
AC005116 Drosophila
AC019704 Drosophila
AE003630 Drosophila
Continuation (3 of 4)
AL596675 Homo sapiens
AF059531 Homo sapiens
AF059531 Homo sapiens
U79286 Human sagittalis
AF007582 Arabidopsis
AC017962 Drosophila
AC007669 Drosophila

3124 bp mRNA ROD 29-JUN-1999
mus protein arginine methyltransferase (CarnI) mRNA,
cds.
1 GI:5257220

use.
Muscululus
Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus
s 1 to 3124)
Ma,H., Hong H., Koh,S.S., Huang,S.M., Schurter,B.T.,
and Stalcup,M.R.
of transcription by a protein methyltransferase
884 (5423), 2174-2177 (1999)

s 1 to 3124)
Ma,H., Hong,H., Koh,S.S., Huang,S., Schurter,B.T.,
and Stalcup,M.R.

Submission
J (05-JAN-1999) Pathology, University of Southern
Alabama, School of Medicine, 2011 Zonal Ave. NHR 301, Alhambra
USA
location/Qualifiers
1. .3124
1. .3124
/organism="Mus musculus"
/db_xref="taxon:10090"
1. .3124
1.gene="Carnl"

[illegible]

QY 721 acagaccgcatcgtgtgtcatcccttggcaaaagtagagagctcatctgtccttagcaagt 780
DB 721 ACAGACCGCATCGTGTGCATCCCTGGCAAAAGTAGAGAGTCTCATTCCTGAGCAAGG 780
QY 781 gaactatcatcttagagcccatgtgtctacatgtctcttcaatgaagaagtctgagagc 840
DB 781 GAACTTATCATCTCAGAGCCCATGGCTACATGCTTCAATGAAAGATGCTCAGAGAC 840
QY 841 taactcatgcaaaaagttacttgaagcttagtgaagcaatgttcccaacatgtgtat 900
DB 841 TAACTCATGCAAAAAGTTACTGAAGCTTAGTGAACATGTTCCCAACATTTGAT 900
QY 901 gtccacatcgcaaccttcaactatgatgaacagcttctacatgtgagcagttcaaccaagccac 960
DB 901 GTCCACCTCGCAACCTTCACTGATGAACAGCTTACATGAGAGTTCACCAAGCCAAC 960
QY 961 ttccggttaacagccatctcttccatgtgaggtgtgacctgtgcctcagaagtgtgcgctgtg 1020
DB 961 TTCGGTAAACAGCCATCCTTCCATGAGTGAAGTGCCTGTGCGCTCAGAGTGCCTGTG 1020
QY 1021 gatgaagtaacttcgagcaacctgtgtggaacacatttgaacatccgagatctcagtagccaa 1080
DB 1021 GATGAGTAACCTTCGCGCAACCTGTGTGAGACATTTGACATCCGATCTCATGAGCCAA 1080
QY 1081 tctgtcaagtaacagagtgaacttcttagaagccaagaagcagattgtcacagagatagaa 1140
DB 1081 TCTGTCAAGTAAACAGTGAAGTCTTAGAAGCCAAAGAGCGATTGTCACAGGATAGAA 1140
QY 1141 atcccatcaaatctcccaatgtgtcatctcaaggtgtatcgaatgtgtgcttctgttctc 1200
DB 1141 ATCCCATCAAAATTCACATGCTGCTCATTCAGGCTAGTGCATGAGCTTGTGCTGCTTC 1200
QY 1201 gatgtgtcttcaatgtgtccataatgaacgtgtgtgtatccagagccccaagagccc 1260
DB 1201 GATGTGTCTTTCANTGTGCTTCATATGACCGTGTGTGCTATCAGCCCAAGAGGCC 1260
QY 1261 ctgaaccaactgtgtacacaggtccgtgtcctcttccagatccgtgtgtgtgtgtgtgtgtgt 1320
DB 1261 CTGACCCACTGTGTACACAGGTCCGGTCCGCTCTTCCAGTACACGTTGTTGCCAAGGCCGG 1320
QY 1321 gaaacgtcttccagaggaagtgtgtgtatgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1380
DB 1321 GAAACGCTCTCAGAGGAATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1380
QY 1381 attgtgtgcaaggtgtgacacagagcttccaaagtccagtaacgtgtgtgtgtgtgtgtgtgt 1440
DB 1381 ATTGTGTGCAAGGTGTGACACAGAGCTCCAAAGTCCAGTAACCTGTGTGTGTGTGTGTGT 1440
QY 1441 cccttcttcaagtaglacaaagttacaacccaacccaacccaacccaacccaacccaacccaac 1500
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VERSION BC003964.1 GI:13278270
KEYWORDS house mouse.
SOURCE Mus musculus
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 2336)
AUTHORS Strausberg, R.
TITLE Direct Submission
JOURNAL Submitted (28-FEB-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
NIH-MGC Project URL: http://mgc.nci.nih.gov
CONTACT: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert.Strausberg@nih.gov
Tissue Procurement: Lohar Hemighausen Ph.D., Robin Humphreys
CDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: The I.M.A.G.E. Consortium (LNL)
Center, Stanford University School of Medicine, Stanford, CA 94305
Web site: http://www-shgc.stanford.edu
Contact: (Dickson, Mark) modpaxi.stanford.edu
Dickson, M., Schmitt, J., Grimwood, J., Rodriguez, A., and Myers,
R. M.

Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LNL at: http://image.lnl.gov
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Location/Qualifiers
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ORIGIN
Query Match 72.2% Score 2256.4; DB 94; Length 2336;
Best Local Similarity 99.3% Pred. No. 0;
Matches 2308; Conservative 0; Mismatches 11; Indels 5; Gaps 4;
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ORGANISM	Mus musculus		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
TITLE	1 (bases 1 to 233830)		
JOURNAL	DOE Joint Genome Institute.		
REFERENCE	Unpublished		
AUTHORS	2 (bases 1 to 233830)		
TITLE	DOE Joint Genome Institute.		
JOURNAL	Direct Submission		
COMMENT	Submitted (29-JUN-2000) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA		
	-----Genome Center		
	Center: Joint Genome Institute		
	Center Code: JGI		
	Web site: http://www.jgi.doe.gov		

	Project Information		
	Center Project Name: 1831860		
	Center clone name: RPC1-23_247F20		

	Summary Statistics		
	Consensus quality: 215926 bases at least Q40		
	Consensus quality: 224967 bases at least Q30		
	Consensus quality: 226764 bases at least Q20		
	Estimated insert size: 225370; agarose-fp estimation		
	Estimated insert size: 231930; sum-of-ctgts estimation		
	Quality coverage: 7.83 in Q20 bases; agarose-fp estimation		
	Quality coverage: 7.61 in Q20 bases; sum-of-ctgts estimation		
	* NOTE: This is a 'working draft' sequence. It currently		
	* consists of 20 contigs. The true order of the pieces		
	* is not known and their order in this sequence record is		
	* arbitrary. Gaps between the contigs are represented as		
	* runs of N, but the exact sizes of the gaps are unknown.		
	* This record will be updated with the finished sequence		
	* as soon as it is available and the accession number will		
	* be preserved.		
	1 1072: contig of 1072 bp in length		
	* 1073 1172: gap of unknown length		
	* 1173 2301: contig of 1129 bp in length		
	* 2302 2401: gap of unknown length		


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ACCESSION AF055027.1 GI:3005756
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS 1 (bases 1 to 2160)
Anderson, B., Wentland, M.A., Ricafrente, J.Y., Liu, W. and Gibbs, R.A.
TITLE A 'double adaptor' method for improved shotgun library construction
JOURNAL Anal. Biochem. 236 (1), 107-113 (1996)
MEDLINE 96207227
REFERENCE 2 (bases 1 to 2160)
Yu, W., Anderson, B., Morley, K.C., Muzny, D.M., Ding, Y., Liu, W.,
AUTHORS Ricafrente, J.Y., Wentland, M.A., Lennon, G. and Gibbs, R.A.
TITLE Large-scale concatenation cDNA sequencing
JOURNAL Genome Res. 7 (4), 353-358 (1997)
MEDLINE 97264341
REFERENCE 3 (bases 1 to 2160)
Yu, W. and Gibbs, R.A.
AUTHORS Direct Submission
JOURNAL Submitted (23-MAR-1998) Molecular and Human Genetics, Baylor
College of Medicine, One Baylor Plaza S930, Houston, TX 77030, USA
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Db 781 GAAACACTGTGGAAACAGGGGACAGCACTTACACCTCAGCAGCGGATGGCGTGGACAGG 840
QY 1567 atgcctactgtcctcagacccctgagcaggtgtatgttcggcgccgtccatgtgtgtgtacac 1626
Db 841 ATGCGCAGCCGCTTATGACTTGACAGATGTTTTCCTGAGTCCAGCGGTGGCCACAC 900
QY 1627 aacctgattcctctagctaaacagaaggtatgtcacaaccccaactcccgatgtgtctcc 1686
Db 901 AACCTGATCTCTTATGACCAACAGGGGATTTGTCAATACACCCACTCCCGGATGGGCTCC 960
QY 1687 ataatagcaagggatgttccaaaggtcctcaaggtcctcaaggtcctcaaggtcctcaag 1743
Db 961 ATATGACGACAGGGGATTTGTCCAAAGGCTCTCCGCGCCAGGACAGTGGTGCGACG 1020
QY 1744 tccagtgcccaatgataagacaaacaaacagttcacaatgagtgccctgcatctctatg 1803
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QY 1804 gctctgcccatgttccatcccgcaacaacacacatgacataggagttagttgtcctccagcc 1863
Db 1081 GCGTCGCCCATGTGTCATCCCGACCAACACCATGACATACGGGACTAGGGGC----- 1132
QY 1864 ggcagacactgtgcacatgcagcaacagaaacaaatcaatgacagc---ccggcac 1920
Db 1133 ----CCGCCCCGGGAGCTGACACACAGGAAACCAATGATGTGCCCGCGGCCGCC 1188
QY 1921 agccagtgctgttcccccctgttcttgagagaagtgtgtgaacacccgttcaagc-ctcc 1979
Db 1189 CGCGGGCGGCTTCCCTTGTGATCTGAGAGAG--CTGCAACACCCCGGTCAACACTCTCT 1246
QY 1980 ttgctatggaacttggacaaatttggacagatgtgcgcgtcgcctcagtaagtaaccoca 2039
Db 1247 TTCTTATGGGAATGGGACACTTTTTCACGATGTTGCGCCCTCCCA---CCCTAAC 1303
QY 2040 gcccaaccttgttcccgacgctgtgtgtgtccataacttaacatgatactgtgtgg 2099
Db 1304 CCCCACTCCCGGCGCTGACAGCTGTGTCGCTGCGCATTTTACACAATAATCATGTTGTGG 1363
QY 2100 cagccctcat--ctgttctgtactcactcactgtacatgctgttgacatctgtgtgaag 2157
Db 1364 GAACCTCTGTCGCCCTCTCTGCGCCGCTTACCTTGACCTGGGCTGTGATCTGTGTGAAC 1423
QY 2158 aggcagagtcctcccccacaccccaagctgcacatgacagcgagggagggagccagcagc 2217

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QY 3124 a 3124
 Db 1114 A 1114

RESULT 6
 LOCUS BC002282/c
 DEFINITION Mus musculus, similar to hypothetical protein, clone MGC:7695, mRNA, complete cds.
 ACCESSION BC002282
 VERSION BC002282.1 GI:12805604
 KEYWORDS MGC.
 SOURCE house mouse.
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 2107)
 Strausberg, R.
 Direct Submission
 Submitted (31-JAN-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA
 NIH-MGC Project URL: <http://mgc.nci.nih.gov>
 Contact: Robert Strausberg, Ph.D.
 Tel: (301) 496-1550
 Email: Robert.Strausberg@nih.gov
 Tissue Procurement: Lothar Hennighausen Ph.D., Robin Humphreys CDNA Library Preparation: Life Technologies, Inc.
 DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Sequencing Group at the Stanford Human Genome Center, Stanford University School of Medicine, Stanford, CA 94305
 Web site: <http://www-shgc.stanford.edu>
 Contact: (Dickson, Mark) modépx11.stanford.edu
 Dickson, M., Schultz, J., Grimwood, J., Rodriguez, A., and Myers, R. M.

REMARK
 COMMENT
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
 Series: IRK Plate: 8 Row: 1 Column: 24.
 Location/Qualifiers
 1. 2107
 /organism="Mus musculus"
 /db_xref="taxon:10090"
 /clone="MGC:7695 IMAGE:3497525"
 /tissue_type="Mammary tumor. WAP-TGF alpha model. 7 months old, gross tissue."
 /clone_1lb="NCI-CGAP_Mam5"
 /lab_host="DH10B"
 /note="Vector: pCMV-SPORT6"
 189..1127
 /codon_start=1
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 /translation="MAADELAFHEFEENATLAEFPDAATTSOSDELSTREHAVVY GSGIGYGAVEGEEDDKTSLOEKRPQPFMTWYDYOSEPDVTSOYIKKSLDPH PGNHVRHHLRNRDLPXGPMFCATLAPLAYGNTLYLAQRDSIRHSPPHKYT IAGITTYCTAMLYPLALMGFLRMKQGTREMGJLYTLEVCVGYGSLFVETPVVLM LITVQWQLFGALGLAAGLFTLMPVREDTRLVAAALSTVLLHALALMGCKL YFQPLPDHVVPAPOATPPSPVLLPSSIQPTWS"

BASE COUNT 447 a 533 c 608 g 519 t
 ORIGIN

Query Match 23.9%; Score 745.8; DB 94; Length 2107;
 Best Local Similarity 98.8%; Pzed. No. 1.9e-150;
 Matches 772; Conservative 0; Mismatches 7; Indels 2; Gaps 2;

QY 2346 tgcgtgttttttaatttttttttttaagaaagacagtgtaaccacagaccctc 2405
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 Db 2092 TGCTGCTTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTT

QY 2406 tgaagaaccggctg-cgcgcgaagccagccccctgtctcctagaccagagttccta 2464
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 Db 2032 TGAGAAACCCGGCTGGCGGGCCAAACGACAGCCCTGTCCTAGGCCAGAGTTCTTA 1973

QY 2465 ggtgaagggtgacctgtcaagccttcagagtgaggacag-ccctcccaacaaaggtt 2523
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 Db 1972 GGTGAGGGGTGGCCCTGTCAAGCCTTCAGAGTGGGCACAGCCCTCCACCAAGGGTT 1913

QY 2524 caccctaaactgaatgtacaaaccccaagctgtccaaagcctgtccctcttctg 2583
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 Db 1912 CACCTCAAACTGAATGTAAACCAACCAACGCTGTCAAAAGGCTGTCTCTCTTTCTG 1853

QY 2584 ctactgtccctcgaagcccgaaagccccctccatcaaaagcttgaaacagagccc 2643
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 Db 1852 CTACGTCTCTGCTCGAGAGCCCTGGAAGCCCTCCATCAAAAGCTTGAACAGGCGCC 1793

QY 2644 agagtgtcaccctggtgactgtgggcagacaagaaccccaaatcctcaaatcgtcaca 2703
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 Db 1792 AGAGTGTACACCTGGGCTACTGGGGCAGACAAAGAACTCAAGATCTGTACACACA 1733

QY 2704 cacaaggaagtgctcctcctcctgatagtcagacatagcctgtgtgttggttcaatca 2763
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 Db 1732 CACAAGGAAGGGCTCTCTCTGTGATAGTAACTAGGCTGTGTGTGGTTCAATTCATCA 1673

QY 2764 tgttacttaactcctcctaagacagaaacccctgggaaggaagcctcgagagaccctccc 2823
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 Db 1672 TGTTTACTTAATCTCTCTCAACAGACACCTGGGAAGAGCTTGACAGGAGCTTCCCC 1613

QY 2824 agacaagaagaagaacaaacaaaggaaggtgattaaataagcagaagcagttccctatt 2883
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 Db 1612 AGACAAGAAGAAGCAAGAAAGGAAGGTGATTAATAGACAGGCAATTTCCCTATT 1553

QY 2884 ccctaccctagagtcgccacctgaatggcagagcctgcagaggaaccccttgcaaa 2943
 |||||||
 Db 1552 CCTTACCTTAGAGTCCCACTCAATGCGCACAGCTTCCACAGAACCCCTTGGCATA 1493

QY 2944 gctggaagctgctgtgtgcacccctcctgaactgttcaagggaatcaaggagccctaa 3003
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 Db 1492 GGCTGAGACTGCTGTGTGACACCTCTGACCTGTGACAGGGAATCAGAGGCTTCAGGCA 1433

QY 3004 gctgggaacaggtctctctcctgtccatgaataactcctgtcgtcgtgaatggccctccc 3063
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 Db 1432 GCTGGGAACAGAGGCTCTCTCTGCTCCATCAGTAATATCTCTTGTCTGCTGCCCCC 1373

QY 3064 cacccttataataatctcctgtgataccttgcataagaataaaagtgttgctttgta 3123
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 Db 1372 CACCTTTATATAATTCCTGTGATCACCCTTGCAATAGAAAATAAAGTGTGCTTTGTA 1313

QY 3124 a 3124
 Db 1312 A 1312

RESULT 7
 LOCUS AX079470
 DEFINITION Sequence 214 from Patent WO0107611.
 ACCESSION AX079470
 VERSION AX079470.1 GI:13159030
 KEYWORDS
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 1 (bases 1 to 500)
 Baker, K.P., Goddard, A. and Wood, W.I.
 Human polypeptides and methods for the use thereof
 Patent: WO 0107611-A 214 01-FEB-2001;
 Genentech, Inc. (US)
 Location/Qualifiers
 1..500
 /organism="Homo sapiens"

BASE COUNT 118 a 149 c 123 g 102 t 8 others
ORIGIN

Query Match 13.1%; Score 409.2; DB 10; Length 500;

Best Local Similarity 88.8%; Pred. No. 8.8e-78; Indels 0; Gaps 0;

Matches 438; Conservative 0; Mismatches 35; Indels 0; Gaps 0;

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DB 8 AATTTTTNAAGCCCAANGAAGAGATTTCACAGATAGAAATCCATTCAATTCACAC 67
QY 1160 tgcctcattcagagctagcctcagctcgtctcgtctcgtctcgtctcgtctcgtct 1219
DB 68 TGTTCATTTCAGGAGGTTGGTTCACAGGAGGTTGGTTCAGGAGGTTGGTTCAGG 127
QY 1220 ccatatgacgctgctgctcctcagcagcagcagcagcagcagcagcagcagcag 1279
DB 128 CCATATATGACCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 187
QY 1280 tccggtgctcttcacagctcgtctgctcagcagcagcagcagcagcagcagcag 1339
DB 188 TGGCGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 247
QY 1340 gctcgtctatctcacaagaagcagcagcagcagcagcagcagcagcagcagcag 1399
DB 248 GTCTCTTATTTCCAAACAAAGACAGATACATATGTGTGTGTGTGTGTGTGTGTGT 307
QY 1400 aagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcag 1459
DB 308 AGACCGGCTCCAAAGTCCATTAACCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 367
QY 1460 gtacaccccatcaccacccacacacacacacacacacacacacacacacacacac 1519
DB 368 GCACAACGCGCTCACCCACCGCGCTCCACATACATCTCCCTGGGAACATGTGGA 427
QY 1520 aacaggaagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcag 1579
DB 428 ACACGGGCGACCTTACACCTCAGCAGCGGATGCGCGGAGGATGCGACCGCT 487
QY 1580 acgagcagcagcag 1592
DB 488 ATGACTTGACGAG 500

RESULT 8
AC013033/c
LOCUS AC013033.1 11218 bp DNA HTG 03-NOV-1999
DEFINITION Drosophila melanogaster, *** SEQUENCING IN PROGRESS ***, in ordered
pieces.

ACCESSION AC013033
VERSION AC013033.1 GI:6223298
KEYWORDS HTG; HTGS_PHASE2.
SOURCE fruit fly.
ORGANISM Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

REFERENCE 1 (bases 1 to 11218)
AUTHORS Adams, M. and Venter, J.C.
TITLE Direct Submission
JOURNAL Submitted (03-NOV-1999) Celera Genomics, 45 West Gude Drive,
Rockville, MD, USA
COMMENT This sequence was identified as CDM:10212601 by the submitter.
For further information on this sequence you may e-mail to
fly@celera.com.

FEATURES
source
1..11218
* NOTE: This is a 'working draft' sequence.
* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.

BASE COUNT 3524 a 2477 c 2429 g 2788 t
ORIGIN

Query Match 13.1%; Score 408; DB 63; Length 11218;

Best Local Similarity 58.9%; Pred. No. 7.6e-78; Indels 57; Gaps 2;

Matches 776; Conservative 0; Mismatches 485; Indels 57; Gaps 2;

QY 269 agtgcctgctcccgagagagagagagagagagagagagagagagagagagagagagag 328
DB 2448 AGTACATGATAGAGCGCGGATAGAGATGCGCCCAATGGAGAGAGATATGCGGTTT 2389
QY 329 cccctgagctgcaacagcgtcctcagctcagctcagctcagctcagctcagctcagct 388
DB 2388 CCGTGGACGCGGACAAATCTGAGGTTGTGACAGCAGACAGACAGCAGCAGCTTTC 2339
QY 389 acaacatccctgaaacacctgctcgagcagcagcagcagcagcagcagcagcagcagcag 448
DB 2328 GCATAAGTGTGAGAGACGTAGACACTTGAACCCAG--TCCGTGTTCTGCGACGCCA 2272
QY 449 cagagagatccctcagctgctgagctcagctcagctcagctcagctcagctcagctcag 508
DB 2271 CTGAGGAGTGTGCTCGCTCCAGTACTTCAAGTTCTAGGCTACTCAGTACGAGCAGA 2212
QY 509 acatgatgacagagactatgctgagcagcagcagcagcagcagcagcagcagcagcagc 568
DB 2211 ACATGATGACGAGACTATGAGGACAAAGACAGCTATGACGCGGCTTCTAAGCAATG 2152
QY 569 cggagctcagagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 628
DB 2151 TGGATTTTCAGGACAAATATGCTCTGATGTGGGCGCGGCTCGGCAATTTCTCTCT 2092
QY 629 ttcgtctcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 688
DB 2091 TTGGCGGTGAGGCGGAGCTGCCAAGTATGAGGCTTGAAGGCTTCAACATGTGGCCAG 2032
QY 689 atgcaagagctcgtgctgagagagagagagagagagagagagagagagagagagagag 748
DB 2031 ACGCCGACGAGCTGTGTGAGTCCAAACATGTGACATATCTGTGTATACCGGGA 1972
QY 749 aagtagagagagagagagagagagagagagagagagagagagagagagagagagagag 808
DB 1971 AGATCGAGAGATGAGCTGCTCCGAGAAAGTGAAGCTTATATATACAGAGCTTATG 1912
QY 809 acatgctctcacaatgaaagcagagagagagagagagagagagagagagagagagagagag 868
DB 1911 ATATGCTGTACAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1852
QY 869 ctatgtaaacatgtcccaacatgtgagagagagagagagagagagagagagagagagag 928
DB 1851 CGCAAGGAAAGATGTACCCACGACGCGGCTTGCACATGACACCTTTTCGGAGCAAT 1792
QY 929 agctctacatgagagagagagagagagagagagagagagagagagagagagagagag 988
DB 1791 CGCTCTCTCTCGAACAATATATATATATATATATATATATATATATATATATATAT 1732
QY 989 tgaagcgtgagcagcagagagagagagagagagagagagagagagagagagagagagag 1048
DB 1731 TTGACCTTACACCGCTGACAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1672
QY 1049 acaatctgacatccgagagagagagagagagagagagagagagagagagagagagagag 1108
DB 1671 ACACCTTGCAGATCCGATATATATATATATATATATATATATATATATATATATAT 1612
QY 1109 aagcacaagaagcagatttcagagagagagagagagagagagagagagagagagagagag 1136
DB 1611 ACGATTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1552
QY 1137 -----agaatcccatcaaatccatccatccatccatccatccatccatccatccatcc 1174
DB 1551 TGGCAACTGTGACTTTCGCGAGGAGATCCCTGAGATTTACATTTCTGCAACTGGCA 1492


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repeat_region complement(5612..5636)
/rpt_family="AT_Rich"
repeat_region 5716..6059
/rpt_family="L1"
repeat_region complement(6107..6260)
/rpt_family="LINE2"
repeat_region complement(6617..6914)
/rpt_family="AluSp"
repeat_region complement(6922..6997)
/rpt_family="MIR"
repeat_region 7157..7456
/rpt_family="AluSc"
repeat_region complement(8320..8426)
/rpt_family="(GCGA)n"
repeat_region complement(8431..8564)
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repeat_region 8568..8694
/rpt_family="LINE2"
repeat_region 8696..8954
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/note="predicted exon, program: graal2exons_human_1.3,
frame: 2, quality: excellent, score: 81.000"
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mammary gland NbMWG Mus musculus CDNA clone 851575 5';
(1..87); 82% identity."
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/note="DBS similarity to AA461913 vf95h04.r1 Soares mouse
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(88..175); 80% identity."
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/rpt_family="AluDo"
repeat_region 10798..10932
/rpt_family="AluSx"
repeat_region 10933..11240
/rpt_family="AluYb8"
repeat_region 11241..11411
/rpt_family="AluSx"
repeat_region complement(11412..11509)
/rpt_family="AluS"
repeat_region 11713..11750
/rpt_family="tRNA-Gln-CAG"
repeat_region complement(11752..12062)
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repeat_region 12175..12307
/rpt_family="AluDo/FLAM"
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repeat_region complement(12525..12595)
/rpt_family="AluSg/X"
repeat_region complement(12596..12830)
/rpt_family="AluSx"
repeat_region complement(12840..13140)
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repeat_region complement(13146..13169)
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/rpt_family="AluSx"
repeat_region complement(14775..15073)
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repeat_region complement(15074..15209)
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frame: 2, quality: excellent, score: 92.000"
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mammary gland NbMWG Mus musculus CDNA clone 851575 5';
(176..264); 73% identity."
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repeat_region 17186..17493
/rpt_family="(GAAA)n"
misc_feature 17562..17589
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(265..292); 75% identity."
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misc_feature 19161..19204
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mammary gland NbMWG Mus musculus CDNA clone 851575 5';
(293..336); 82% identity."
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Best Local Similarity 90.2%; Pred No. 3.3e-34;
Matches 231; Conservative 0; Mismatches 22; Indels 3; Gaps 1;
QY 3 gggagcgtgagccgacctaagaatgagcagcgagcagcgagcgtggtggccgggtgc 62
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DB 30927 GGGCGCTGAGCGGATCTAAGATGCGACGCGCGCGG---CGGCGGTGGCGCGCGCG 30983
QY 63 gggagcgtggtgtggtggcgcccgagcgagcgagcgagcgtggtgtgtt 122
|||||
DB 30984 GGGCGCGCGCGGCGGCTGCGCGTCCCGCGCGCGCGCGCGCGTGTGCGGT 31043
QY 123 cccggagcgccgctccctactatcgagcagcgagcagcgagatccagcgagcgag 182
|||||
DB 31044 CCCGCGCGCGCGCTCTCAACATCGCGACGCGAAGCGCGAGATCCAGCGGACGCGGA 31103
QY 183 gtagcagcgctgctgaggtggtggtggtggtggtggtggtggtggtggtggtggt 242
|||||
DB 31104 GAGCAGCGGCGGCGCGCTGAGAGTGGCGCGCGCGCGGCGGACTGCGCGGCGATCCCTCTA 31163

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Query Match	Best Local Similarity	Matches	188; Conservative	5.5%; Score 171; DB 75; Length 233830; 94.5%; Pred. No. 4.3e-27; 0; Mismatches 10; Indels 1; Gaps 1
QY 677	ccatgctcgaacatgcagaggtcctcggtggaagatgaacaatctgacagaccgcatctgtg	736		
Db 106828	CCTTCTCCCACTCTCTACAGGTCCCTGGTGAAGAAGTACATCTGACAGACCCGATGTGG	106769		
QY 737	tcatccctcgtgcaaaagtagagagaggtcctatctgccctgaggaagctgacatlatcatctcag	796		
Db 106768	TCAT-CCTGGCAAGATAGAGAGAGGTCTCATTCCTCGAGCAAGTGACATTATCATCTCAG	106710		
QY 797	agcccatcgtggtctacatgctcttccatgaacgaagtctcgtgagagctaccctccacgcaaaa	856		
Db 106709	AGCCCATGGGTACTACATGCTCTCAATGAACGAATGCTCGAGAGCTTACCTCCATGCCAAAA	106650		
QY 857	agtaccctgaagcctagctagtg	875		
Db 106649	AGTACCTGAAGCCTTAGTGG	106631		
RESULT 15	AF263539			
LOCUS	AF263539	1173 bp	mRNA	PRI 10-AUG-2000
DEFINITION	Homo sapiens arginine N-methyltransferase (HRMT1L3) mRNA, complete cds.			
ACCESSION	AF263539			
VERSION	AF263539.1			
KEYWORDS	GI:9652073			
SOURCE	human.			
ORGANISM	Homo sapiens			
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
AUTHORS	1 (bases 1 to 1173)			
TITLE	Lorenz,B. and Strom,T.M.			
JOURNAL	Transcripts in human map region 12p13.3			
REFERENCE	unpublished			
AUTHORS	2 (bases 1 to 1173)			
JOURNAL	Strom,T.M.			
REFERENCE	Direct Submission			
TITLE	Submitted (03-MAY-2000)			
JOURNAL	Muenchen 80336, Germany			
COMMENT	Predicted by homology to the arginine N-methyltransferase gene 1. The predicted exons were confirmed by RT-PCR using brain cDNA. The entry contains the complete coding sequence. The 3'-UTR may be incomplete.			

* * * * * STN Columbus * * * * *

FILE 'HOME' ENTERED AT 09:38:09 ON 21 JUN 2001

=> fil .bec

COST IN U.S. DOLLARS

SINCE FILE	TOTAL
ENTRY	SESSION

FULL ESTIMATED COST

0.30	0.30
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FILES 'MEDLINE, SCISEARCH, LIFESCI, BIOTECHDS, BIOSIS, EMBASE, HCAPLUS, NTIS, ESBIODBASE, BIOTECHNO, WPIDS' ENTERED AT 09:39:14 ON 21 JUN 2001
ALL COPYRIGHTS AND RESTRICTIONS APPLY. SEE HELP USAGETERMS FOR DETAILS.

11 FILES IN THE FILE LIST

=> s arginine methyltransferase#

FILE 'MEDLINE'

51900 ARGININE

12238 METHYLTRANSFERASE#

L1 50 ARGININE METHYLTRANSFERASE#
(ARGININE (W) METHYLTRANSFERASE#)

FILE 'SCISEARCH'

43003 ARGININE

8352 METHYLTRANSFERASE#

L2 55 ARGININE METHYLTRANSFERASE#
(ARGININE (W) METHYLTRANSFERASE#)

FILE 'LIFESCI'

12502 "ARGININE"

3436 METHYLTRANSFERASE#

L3 28 ARGININE METHYLTRANSFERASE#
("ARGININE" (W) METHYLTRANSFERASE#)

FILE 'BIOTECHDS'

1250 ARGININE

345 METHYLTRANSFERASE#

L4 1 ARGININE METHYLTRANSFERASE#
(ARGININE (W) METHYLTRANSFERASE#)

FILE 'BIOSIS'

61402 ARGININE

9218 METHYLTRANSFERASE#

L5 44 ARGININE METHYLTRANSFERASE#
(ARGININE (W) METHYLTRANSFERASE#)

FILE 'EMBASE'

46360 "ARGININE"

9178 METHYLTRANSFERASE#

L6 66 ARGININE METHYLTRANSFERASE#
("ARGININE" (W) METHYLTRANSFERASE#)

FILE 'HCAPLUS'

83188 ARGININE

11288 METHYLTRANSFERASE#

L7 79 ARGININE METHYLTRANSFERASE#
(ARGININE (W) METHYLTRANSFERASE#)

FILE 'NTIS'

288 ARGININE
35 METHYLTRANSFERASE#
L8 0 ARGININE METHYLTRANSFERASE#
(ARGININE (W) METHYLTRANSFERASE#)

FILE 'ESBIOBASE'
16076 ARGININE
2647 METHYLTRANSFERASE#
L9 32 ARGININE METHYLTRANSFERASE#
(ARGININE (W) METHYLTRANSFERASE#)

FILE 'BIOTECHNO'
14229 ARGININE
3989 METHYLTRANSFERASE#
L10 43 ARGININE METHYLTRANSFERASE#
(ARGININE (W) METHYLTRANSFERASE#)

FILE 'WPIDS'
4144 ARGININE
194 METHYLTRANSFERASE#
L11 2 ARGININE METHYLTRANSFERASE#
(ARGININE (W) METHYLTRANSFERASE#)

TOTAL FOR ALL FILES
L12 400 ARGININE METHYLTRANSFERASE#

=> s l12 and (gene/q or mouse or murine)

FILE 'MEDLINE'
210763 MOUSE
89759 MURINE
L13 35 L1 AND (GENE/Q OR MOUSE OR MURINE)

FILE 'SCISEARCH'
219978 MOUSE
92269 MURINE
L14 37 L2 AND (GENE/Q OR MOUSE OR MURINE)

FILE 'LIFESCI'
84682 MOUSE
41177 MURINE
L15 22 L3 AND (GENE/Q OR MOUSE OR MURINE)

FILE 'BIOTECHDS'
18663 MOUSE
1364 MURINE
L16 1 L4 AND (GENE/Q OR MOUSE OR MURINE)

FILE 'BIOSIS'
586309 MOUSE
120340 MURINE
L17 32 L5 AND (GENE/Q OR MOUSE OR MURINE)

FILE 'EMBASE'
461645 MOUSE
83778 MURINE
L18 43 L6 AND (GENE/Q OR MOUSE OR MURINE)

FILE 'HCAPLUS'
242778 MOUSE

82230 MURINE
L19 43 L7 AND (GENE/Q OR MOUSE OR MURINE)

FILE 'NTIS'

3632 MOUSE
-831 MURINE
L20 0 L8 AND (GENE/Q OR MOUSE OR MURINE)

FILE 'ESBIOBASE'

63068 MOUSE
28856 MURINE
L21 22 L9 AND (GENE/Q OR MOUSE OR MURINE)

FILE 'BIOTECHNO'

181746 MOUSE
47727 MURINE
L22 30 L10 AND (GENE/Q OR MOUSE OR MURINE)

FILE 'WPIDS'

13615 MOUSE
2010 MURINE
L23 1 L11 AND (GENE/Q OR MOUSE OR MURINE)

TOTAL FOR ALL FILES

L24 266 L12 AND (GENE/Q OR MOUSE OR MURINE)

=> s (steroid or glucocorticoid) (w) receptor#

FILE 'MEDLINE'

64982 STEROID
19511 GLUCOCORTICOID
510798 RECEPTOR#
L25 8873 (STEROID OR GLUCOCORTICOID) (W) RECEPTOR#

FILE 'SCISEARCH'

46748 STEROID
19635 GLUCOCORTICOID
528061 RECEPTOR#
L26 11582 (STEROID OR GLUCOCORTICOID) (W) RECEPTOR#

FILE 'LIFESCI'

10489 STEROID
5093 GLUCOCORTICOID
173350 RECEPTOR#
L27 2854 (STEROID OR GLUCOCORTICOID) (W) RECEPTOR#

FILE 'BIOTECHDS'

2021 STEROID
212 GLUCOCORTICOID
8587 RECEPTOR#
L28 131 (STEROID OR GLUCOCORTICOID) (W) RECEPTOR#

FILE 'BIOSIS'

75066 STEROID
22845 GLUCOCORTICOID
601962 RECEPTOR#
L29 10689 (STEROID OR GLUCOCORTICOID) (W) RECEPTOR#

FILE 'EMBASE'

78988 STEROID

29065 GLUCOCORTICOID
 574638 RECEPTOR#
 L30 10565 (STEROID OR GLUCOCORTICOID) (W) RECEPTOR#

 FILE 'HCAPLUS'
 86246 STEROID
 22195 GLUCOCORTICOID
 520156 RECEPTOR#
 L31 10888 (STEROID OR GLUCOCORTICOID) (W) RECEPTOR#

 FILE 'NTIS'
 538 STEROID
 101 GLUCOCORTICOID
 5282 RECEPTOR#
 L32 61 (STEROID OR GLUCOCORTICOID) (W) RECEPTOR#

 FILE 'ESBIOBASE'
 14003 STEROID
 5447 GLUCOCORTICOID
 176734 RECEPTOR#
 L33 3086 (STEROID OR GLUCOCORTICOID) (W) RECEPTOR#

 FILE 'BIOTECHNO'
 15848 STEROID
 7770 GLUCOCORTICOID
 165803 RECEPTOR#
 L34 4460 (STEROID OR GLUCOCORTICOID) (W) RECEPTOR#

 FILE 'WPIDS'
 6368 STEROID
 745 GLUCOCORTICOID
 27056 RECEPTOR#
 L35 202 (STEROID OR GLUCOCORTICOID) (W) RECEPTOR#

 TOTAL FOR ALL FILES
 L36 63391 (STEROID OR GLUCOCORTICOID) (W) RECEPTOR#

 => s transcription?(10a) (activat? or coactivat?)
 FILE 'MEDLINE'
 178258 TRANSCRIPTION?
 470972 ACTIVAT?
 2149 COACTIVAT?
 L37 26684 TRANSCRIPTION?(10A) (ACTIVAT? OR COACTIVAT?)

 FILE 'SCISEARCH'
 151275 TRANSCRIPTION?
 542620 ACTIVAT?
 2966 COACTIVAT?
 L38 30177 TRANSCRIPTION?(10A) (ACTIVAT? OR COACTIVAT?)

 FILE 'LIFESCI'
 82980 TRANSCRIPTION?
 166374 ACTIVAT?
 1276 COACTIVAT?
 L39 17797 TRANSCRIPTION?(10A) (ACTIVAT? OR COACTIVAT?)

 FILE 'BIOTECHDS'
 9484 TRANSCRIPTION?
 16193 ACTIVAT?

15 COACTIVAT?
L40 750 TRANSCRIPTION?(10A) (ACTIVAT? OR COACTIVAT?)

FILE 'BIOSIS'

183345 TRANSCRIPTION?

532844 ACTIVAT?

2255 COACTIVAT?

L41 30083 TRANSCRIPTION?(10A) (ACTIVAT? OR COACTIVAT?)

FILE 'EMBASE'

151019 TRANSCRIPTION?

454821 ACTIVAT?

2072 COACTIVAT?

L42 24630 TRANSCRIPTION?(10A) (ACTIVAT? OR COACTIVAT?)

FILE 'HCAPLUS'

190478 TRANSCRIPTION?

907705 ACTIVAT?

2745 COACTIVAT?

L43 36419 TRANSCRIPTION?(10A) (ACTIVAT? OR COACTIVAT?)

FILE 'NTIS'

1959 TRANSCRIPTION?

26383 ACTIVAT?

42 COACTIVAT?

L44 161 TRANSCRIPTION?(10A) (ACTIVAT? OR COACTIVAT?)

FILE 'ESBIOBASE'

82361 TRANSCRIPTION?

175017 ACTIVAT?

1544 COACTIVAT?

L45 17461 TRANSCRIPTION?(10A) (ACTIVAT? OR COACTIVAT?)

FILE 'BIOTECHNO'

124120 TRANSCRIPTION?

180986 ACTIVAT?

1291 COACTIVAT?

L46 20059 TRANSCRIPTION?(10A) (ACTIVAT? OR COACTIVAT?)

FILE 'WPIDS'

7443 TRANSCRIPTION?

189402 ACTIVAT?

219 COACTIVAT?

L47 747 TRANSCRIPTION?(10A) (ACTIVAT? OR COACTIVAT?)

TOTAL FOR ALL FILES

L48 204968 TRANSCRIPTION?(10A) (ACTIVAT? OR COACTIVAT?)

=> s (l36 or l48) and methyltransferase#

FILE 'MEDLINE'

12238 METHYLTRANSFERASE#

L49 129 (L25 OR L37) AND METHYLTRANSFERASE#

FILE 'SCISEARCH'

8352 METHYLTRANSFERASE#

L50 141 (L26 OR L38) AND METHYLTRANSFERASE#

FILE 'LIFESCI'

3436 METHYLTRANSFERASE#

L51 58 (L27 OR L39) AND METHYLTRANSFERASE#

FILE 'BIOTECHDS'

345 METHYLTRANSFERASE#

L52 0 (L28 OR L40) AND METHYLTRANSFERASE#

FILE 'BIOSIS'

9218 METHYLTRANSFERASE#

L53 109 (L29 OR L41) AND METHYLTRANSFERASE#

FILE 'EMBASE'

9178 METHYLTRANSFERASE#

L54 112 (L30 OR L42) AND METHYLTRANSFERASE#

FILE 'HCAPLUS'

11288 METHYLTRANSFERASE#

L55 146 (L31 OR L43) AND METHYLTRANSFERASE#

FILE 'NTIS'

35 METHYLTRANSFERASE#

L56 0 (L32 OR L44) AND METHYLTRANSFERASE#

FILE 'ESBIOBASE'

2647 METHYLTRANSFERASE#

L57 56 (L33 OR L45) AND METHYLTRANSFERASE#

FILE 'BIOTECHNO'

3989 METHYLTRANSFERASE#

L58 78 (L34 OR L46) AND METHYLTRANSFERASE#

FILE 'WPIDS'

194 METHYLTRANSFERASE#

L59 0 (L35 OR L47) AND METHYLTRANSFERASE#

TOTAL FOR ALL FILES

L60 829 (L36 OR L48) AND METHYLTRANSFERASE#

=> s (l36 or l48) (10a)methyltransferase#

FILE 'MEDLINE'

12238 METHYLTRANSFERASE#

L61 17 (L25 OR L37) (10A)METHYLTRANSFERASE#

FILE 'SCISEARCH'

8352 METHYLTRANSFERASE#

L62 19 (L26 OR L38) (10A)METHYLTRANSFERASE#

FILE 'LIFESCI'

3436 METHYLTRANSFERASE#

L63 14 (L27 OR L39) (10A)METHYLTRANSFERASE#

FILE 'BIOTECHDS'

345 METHYLTRANSFERASE#

L64 0 (L28 OR L40) (10A)METHYLTRANSFERASE#

FILE 'BIOSIS'

9218 METHYLTRANSFERASE#

L65 23 (L29 OR L41) (10A)METHYLTRANSFERASE#

FILE 'EMBASE'

9178 METHYLTRANSFERASE#
L66 17 (L30 OR L42) (10A) METHYLTRANSFERASE#

FILE 'HCAPLUS'
11288 METHYLTRANSFERASE#
L67 33 (L31 OR L43) (10A) METHYLTRANSFERASE#

FILE 'NTIS'
35 METHYLTRANSFERASE#
L68 0 (L32 OR L44) (10A) METHYLTRANSFERASE#

FILE 'ESBIOBASE'
2647 METHYLTRANSFERASE#
L69 9 (L33 OR L45) (10A) METHYLTRANSFERASE#

FILE 'BIOTECHNO'
3989 METHYLTRANSFERASE#
L70 8 (L34 OR L46) (10A) METHYLTRANSFERASE#

FILE 'WPIDS'
194 METHYLTRANSFERASE#
L71 0 (L35 OR L47) (10A) METHYLTRANSFERASE#

TOTAL FOR ALL FILES
L72 140 (L36 OR L48) (10A) METHYLTRANSFERASE#

=> s (124 or 172) not 2000-2001/py

FILE 'MEDLINE'
548588 2000-2001/PY
L73 32 (L13 OR L61) NOT 2000-2001/PY

FILE 'SCISEARCH'
1314665 2000-2001/PY
L74 35 (L14 OR L62) NOT 2000-2001/PY

FILE 'LIFESCI'
105420 2000-2001/PY
L75 24 (L15 OR L63) NOT 2000-2001/PY

FILE 'BIOTECHDS'
17561 2000-2001/PY
L76 0 (L16 OR L64) NOT 2000-2001/PY

FILE 'BIOSIS'
675341 2000-2001/PY
L77 36 (L17 OR L65) NOT 2000-2001/PY

FILE 'EMBASE'
590226 2000-2001/PY
L78 39 (L18 OR L66) NOT 2000-2001/PY

FILE 'HCAPLUS'
1312271 2000-2001/PY
L79 45 (L19 OR L67) NOT 2000-2001/PY

FILE 'NTIS'
0 2000-2001/PY
L80 0 (L20 OR L68) NOT 2000-2001/PY

FILE 'ESBIOBASE'
378889 2000-2001/PY
L81 16 (L21 OR L69) NOT 2000-2001/PY

FILE 'BIOTECHNO'
160069 2000-2001/PY
L82 22 (L22 OR L70) NOT 2000-2001/PY

FILE 'WPIDS'
1212346 2000-2001/PY
L83 0 (L23 OR L71) NOT 2000-2001/PY

TOTAL FOR ALL FILES
L84 249 (L24 OR L72) NOT 2000-2001/PY

=> dup rem l84
PROCESSING COMPLETED FOR L84
L85 76 DUP REM L84 (173 DUPLICATES REMOVED)

=> d tot

L85 ANSWER 1 OF 76 MEDLINE
TI How chromatin changes its shape.
SO SCIENCE, (1999 Aug 20) 285 (5431) 1200-1, 1203.
Journal code: UJ7; 0404511. ISSN: 0036-8075.
AU Hagmann M
AN 1999408060 MEDLINE

L85 ANSWER 2 OF 76 HCAPLUS COPYRIGHT 2001 ACS
TI Mammalian gene CRX characterization and applications for the detection and treatment of retinal degenerative disease
SO PCT Int. Appl., 147 pp.
CODEN: PIXXD2
IN Freund, Carol L.; McInnes, Roderick R.; Looser, Jens; Cepko, Constance L.; Furukawa, Takahisa; Morrow, Eric M.
AN 1999:350679 HCAPLUS
DN 131:1463

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 9925721	A1	19990527	WO 1998-US24322	19981113
W: AU, CA, JP, NZ, US				
RW: AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE				
AU 9914089	A1	19990607	AU 1999-14089	19981113

L85 ANSWER 3 OF 76 MEDLINE DUPLICATE 1
TI Inhibition of DNA **methyltransferase** stimulates the expression of signal transducer and **activator** of **transcription** 1, 2, and 3 genes in colon tumor cells.
SO PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE UNITED STATES OF AMERICA, (1999 Nov 23) 96 (24) 14007-12.
Journal code: PV3; 7505876. ISSN: 0027-8424.
AU Karpf A R; Peterson P W; Rawlins J T; Dalley B K; Yang Q; Albertsen H; Jones D A
AN 2000040667 MEDLINE

L85 ANSWER 4 OF 76 MEDLINE DUPLICATE 2
TI Unusual sites of arginine methylation in Poly(A)-binding protein II and in vitro methylation by protein **arginine methyltransferases**

PRMT1 and PRMT3.

SO JOURNAL OF BIOLOGICAL CHEMISTRY, (1999 May 7) 274 (19) 13229-34.

Journal code: HIV; 2985121R. ISSN: 0021-9258.

AU Smith J J; Rucknagel K P; Schierhorn A; Tang J; Nemeth A; Linder M;
Herschman H R; Wahle E

AN 1999240708 MEDLINE

L85 ANSWER 5 OF 76 HCAPLUS COPYRIGHT 2001 ACS

TI Analysis of mice carrying targeted mutations of the glucocorticoid
receptor gene argues against an essential role of glucocorticoid
signalling for generating adrenal chromaffin cells

SO Development (Cambridge, U. K.) (1999), 126(13), 2935-2944

CODEN: DEVPED; ISSN: 0950-1991

AU Finotto, Susetta; Krieglstein, Kerstin; Schober, Andreas; Deimling,
Frauke; Lindner, Karin; Bruhl, Barbara; Beier, Konstantin; Metz, Jurgen;
Garcia-Ararras, Jose E.; Roig-Lopez, Jose L.; Monaghan, Paula; Schmid,
Wolfgang; Cole, Timothy J.; Kellendonk, Christoph; Tronche, Francois;
Schutz, Gunther; Unsicker, Klaus

AN 1999:492464 HCAPLUS

DN 131:252700

L85 ANSWER 6 OF 76 MEDLINE

DUPLICATE 3

TI Regulation of transcription by a protein methyltransferase.

SO SCIENCE, (1999 Jun 25) 284 (5423) 2174-7.

Journal code: UJ7; 0404511. ISSN: 0036-8075.

AU Chen D; Ma H; Hong H; Koh S S; Huang S M; Schurter B T; Aswad D W;
Stallcup M R

AN 1999316081 MEDLINE

L85 ANSWER 7 OF 76 MEDLINE

DUPLICATE 4

TI S-Adenosylmethionine-dependent methylation in Saccharomyces cerevisiae.
Identification of a novel protein arginine
methyltransferase.

SO JOURNAL OF BIOLOGICAL CHEMISTRY, (1999 Jan 8) 274 (2) 814-24.

Journal code: HIV; 2985121R. ISSN: 0021-9258.

AU Niewmierzycka A; Clarke S

AN 1999091619 MEDLINE

L85 ANSWER 8 OF 76 HCAPLUS COPYRIGHT 2001 ACS

TI Activation of human O6-methylguanine-DNA methyltransferase gene by
glucocorticoid hormone

SO Oncogene (1999), 18(2), 525-532

CODEN: ONCNES; ISSN: 0950-9232

AU Biswas, Tapan; Ramana, Chilakamarti V.; Srinivasan, Ganesan; Boldogh,
Istvan; Hazra, Tapas K.; Chen, Zhenping; Tano, Keizo; Thompson, E. Brad;
Mitra, Sankar

AN 1999:117843 HCAPLUS

DN 130:276964

L85 ANSWER 9 OF 76 SCISEARCH COPYRIGHT 2001 ISI (R)

TI RNase treatment of yeast and mammalian cell extracts affects in vitro
substrate methylation by type I protein arginine N-methyltransferases

SO BIOCHEMICAL AND BIOPHYSICAL RESEARCH COMMUNICATIONS, (7 JUN 1999) Vol.
259, No. 2, pp. 391-400.

Publisher: ACADEMIC PRESS INC, 525 B ST, STE 1900, SAN DIEGO, CA
92101-4495.

ISSN: 0006-291X.

AU Frankel A; Clarke S (Reprint)

AN 1999:478606 SCISEARCH

- L85 ANSWER 10 OF 76 EMBASE COPYRIGHT 2001 ELSEVIER SCI. B.V.
 TI [Mechanisms of BTG2 activity, a transcriptional target of p53: Evidences and hypothesis].
 MECANISMES D'ACTION DE BTG2, **GENE** CIBLE DE P53: DONNEES ACQUISES ET HYPOTHESES.
 SO Bulletin du Cancer, (1999) 86/4 (358-364).
 Refs: 42
 ISSN: 0007-4551 CODEN: BUCABS
 AU Puisieux A.; Magaud J.-P.
 AN 1999174896 EMBASE
- L85 ANSWER 11 OF 76 MEDLINE DUPLICATE 5
 TI Arginine methylation and binding of Hrp1p to the efficiency element for mRNA 3'-end formation.
 SO RNA, (1999 Feb) 5 (2) 272-80.
 Journal code: CHB; 9509184. ISSN: 1355-8382.
 AU Valentini S R; Weiss V H; Silver P A
 AN 1999146783 MEDLINE
- L85 ANSWER 12 OF 76 SCISEARCH COPYRIGHT 2001 ISI (R)
 TI Identification and characterization of a novel mammalian CpG binding **transcriptional activator** that shares a motif with DNA **methyltransferase** and HRX proteins.
 SO EXPERIMENTAL HEMATOLOGY, (JUL 1999) Vol: 27, No. 7, Supp: [1], pp. 61-61.
 Publisher: ELSEVIER SCIENCE INC, 655 AVENUE OF THE AMERICAS, NEW YORK, NY 10010.
 ISSN: 0301-472X.
 AU Voo K S (Reprint); Carlone D L; Jacobsen B M; Flodin A; Skalnik D G
 AN 1999:528880 SCISEARCH
- L85 ANSWER 13 OF 76 HCAPLUS COPYRIGHT 2001 ACS
 TI Neural regulation of phenylethanolamine N-methyltransferase (PNMT) gene expression in bovine chromaffin cells differs from other catecholamine enzyme genes.
 SO J. Mol. Neurosci. (1999), 12(1), 53-68
 CODEN: JMNEES; ISSN: 0895-8696
 AU Lee, Ying-Shuan-Eda; Raia, Gabrielle; Tonshoff, Christianne; Evinger, Marian J.
 AN 1999:592097 HCAPLUS
 DN 131:347371
- L85 ANSWER 14 OF 76 MEDLINE DUPLICATE 6
 TI delta-N-methylarginine is a novel posttranslational modification of arginine residues in yeast proteins.
 SO JOURNAL OF BIOLOGICAL CHEMISTRY, (1998 Nov 6) 273 (45) 29283-6.
 Journal code: HIV; 2985121R. ISSN: 0021-9258.
 AU Zobel-Thropp P; Gary J D; Clarke S
 AN 1999009026 MEDLINE
- L85 ANSWER 15 OF 76 MEDLINE DUPLICATE 7
 TI Identification of protein-arginine N-methyltransferase as 10-formyltetrahydrofolate dehydrogenase.
 SO JOURNAL OF BIOLOGICAL CHEMISTRY, (1998 Oct 16) 273 (42) 27374-82.
 Journal code: HIV; 2985121R. ISSN: 0021-9258.
 AU Kim S; Park G H; Joo W A; Paik W K; Cook R J; Williams K R
 AN 1998438510 MEDLINE
- L85 ANSWER 16 OF 76 MEDLINE DUPLICATE 8

TI PRMT 3, a type I protein arginine N-methyltransferase that differs from
 PRMT1 in its oligomerization, subcellular localization, substrate
 specificity, and regulation.
 SO JOURNAL OF BIOLOGICAL CHEMISTRY, (1998 Jul 3) 273 (27) 16935-45.
 Journal code: HIV; 2985121R. ISSN: 0021-9258.
 AU Tang J; Gary J D; Clarke S; Herschman H R
 AN 1998307932 MEDLINE

L85 ANSWER 17 OF 76 HCAPLUS COPYRIGHT 2001 ACS
 TI C-Fos deficiency inhibits induction of mRNA for some, but not all,
 neurotransmitter biosynthetic enzymes by immobilization stress
 SO J. Neurochem. (1998), 70(5), 1935-1940
 CODEN: JONRA9; ISSN: 0022-3042
 AU Serova, Lidia I.; Saez, Enrique; Spiegelman, Bruce M.; Sabban, Esther L.
 AN 1998:270959 HCAPLUS
 DN 129:26592

L85 ANSWER 18 OF 76 EMBASE COPYRIGHT 2001 ELSEVIER SCI. B.V.DUPLICATE 9
 TI Enzymatic methylation of recombinant TIS21 protein-arginine residues.
 SO Biochemistry and Molecular Biology International, (1998) 45/5 (871-878).
 Refs: 26
 ISSN: 1039-9712 CODEN: BMBIES
 AU Lim I.K.; Park T.-J.; Kim S.; Lee H.W.; Paik W.K.
 AN 1998311260 EMBASE

L85 ANSWER 19 OF 76 MEDLINE DUPLICATE 10
 TI p53 is involved in regulation of the DNA repair gene O6-methylguanine-DNA
 methyltransferase (MGMT) by DNA damaging agents.
 SO ONCOGENE, (1998 Aug 20) 17 (7) 845-51.
 Journal code: ONC; 8711562. ISSN: 0950-9232.
 AU Grombacher T; Eichhorn U; Kaina B
 AN 1998451281 MEDLINE

L85 ANSWER 20 OF 76 HCAPLUS COPYRIGHT 2001 ACS
 TI The 4S benzo(a)pyrene-binding protein is not a transcriptional activator
 of Cypl1 gene in Ah receptor-deficient (AHR -/-) transgenic mice
 SO Arch. Biochem. Biophys. (1998), 349(2), 349-355
 CODEN: ABBIA4; ISSN: 0003-9861
 AU Foussat, Julie; Costet, Philippe; Galtier, Pierre; Pineau, Thierry; Lesca,
 Pierre
 AN 1998:53563 HCAPLUS
 DN 128:163820

L85 ANSWER 21 OF 76 MEDLINE DUPLICATE 11
 TI Identification and characterization of two putative human **arginine
 methyltransferases** (HRMT1L1 and HRMT1L2).
 SO GENOMICS, (1998 Mar 15) 48 (3) 330-40.
 Journal code: GEN; 8800135. ISSN: 0888-7543.
 AU Scott H S; Antonarakis S E; Lalioti M D; Rossier C; Silver P A; Henry M F
 AN 1998207248 MEDLINE

L85 ANSWER 22 OF 76 MEDLINE DUPLICATE 12
 TI Phenylethanolamine N-methyltransferase gene expression: synergistic
 activation by Egr-1, AP-2 and the glucocorticoid receptor.
 SO BRAIN RESEARCH. MOLECULAR BRAIN RESEARCH, (1998 Oct 30) 61 (1-2) 154-61.
 Journal code: MBR; 8908640. ISSN: 0169-328X.
 AU Wong D L; Siddall B J; Ebert S N; Bell R A; Her S
 AN 1999013984 MEDLINE

L85 ANSWER 23 OF 76 HCAPLUS COPYRIGHT 2001 ACS
 TI Neural control of phenylethanolamine-N-methyltransferase via cholinergic activation of Egr-I
 SO Adv. Pharmacol. (San Diego) (1998), 42(Catecholamines), 77-81
 CODEN: ADPHEL; ISSN: 1054-3589
 AU Wong, Dona L.; Ebert, Steven N.; Morita, Kyoji
 AN 1997:711960 HCAPLUS
 DN 128:631

L85 ANSWER 24 OF 76 HCAPLUS COPYRIGHT 2001 ACS
 TI RNA and protein interactions modulated by protein arginine methylation
 SO Prog. Nucleic Acid Res. Mol. Biol. (1998), 61, 65-131
 CODEN: PNMBAF; ISSN: 0079-6603
 AU Gary, Jonathan D.; Clarke, Steven
 AN 1999:1415 HCAPLUS
 DN 130:193393

L85 ANSWER 25 OF 76 MEDLINE DUPLICATE 13
 TI Protein N-arginine methylation in adenosine dialdehyde-treated lymphoblastoid cells.
 SO ARCHIVES OF BIOCHEMISTRY AND BIOPHYSICS, (1998 Mar 1) 351 (1) 53-9.
 Journal code: 6SK; 0372430. ISSN: 0003-9861.
 AU Li C; Ai L S; Lin C H; Hsieh M; Li Y C; Li S Y
 AN 1998162641 MEDLINE

L85 ANSWER 26 OF 76 MEDLINE DUPLICATE 14
 TI Construction of a 2.5-Mb integrated physical and **gene** map of distal 21q22.3.
 SO GENOMICS, (1998 Apr 1) 49 (1) 1-13.
 Journal code: GEN; 8800135. ISSN: 0888-7543.
 AU Lapenta V; Sossi V; Gosset P; Vayssettes C; Vitali T; Rabatel N; Tassone F; Blouin J L; Scott H S; Antonarakis S E; Creau N; Brahe C
 AN 1998234538 MEDLINE

L85 ANSWER 27 OF 76 MEDLINE DUPLICATE 15
 TI Identification of N(G)-methylarginine residues in human heterogeneous RNP protein A1: Phe/Gly-Gly-Gly-Arg-Gly-Gly-Gly/Phe is a preferred recognition motif.
 SO BIOCHEMISTRY, (1997 Apr 29) 36 (17) 5185-92.
 Journal code: A0G; 0370623. ISSN: 0006-2960.
 AU Kim S; Merrill B M; Rajpurohit R; Kumar A; Stone K L; Papov V V; Schneiders J M; Szer W; Wilson S H; Paik W K; Williams K R
 AN 97282571 MEDLINE

L85 ANSWER 28 OF 76 HCAPLUS COPYRIGHT 2001 ACS
 TI A putative leucine zipper activator of Pasteurella haemolytica leukotoxin transcription and the potential for modulation of its synthesis by slipped-strand mispairing
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 CODEN: INFIBR; ISSN: 0019-9567
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L85 ANSWER 29 OF 76 MEDLINE DUPLICATE 16
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Journal code: DD8; 0425076. ISSN: 0305-1870.

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L85 ANSWER 30 OF 76 SCISEARCH COPYRIGHT 2001 ISI (R)

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CODEN: MAMGEC; ISSN: 0938-8990

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L85 ANSWER 32 OF 76 EMBASE COPYRIGHT 2001 ELSEVIER SCI. B.V.DUPLICATE 17

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L85 ANSWER 33 OF 76 MEDLINE

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L85 ANSWER 34 OF 76 MEDLINE

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L85 ANSWER 38 OF 76 HCAPLUS COPYRIGHT 2001 ACS

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L85 ANSWER 40 OF 76 HCAPLUS COPYRIGHT 2001 ACS

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L85 ANSWER 41 OF 76 BIOSIS COPYRIGHT 2001 BIOSIS

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L85 ANSWER 45 OF 76 EMBASE COPYRIGHT 2001 ELSEVIER SCI. B.V. DUPLICATE 26
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L85 ANSWER 48 OF 76 BIOSIS COPYRIGHT 2001 BIOSIS
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L85 ANSWER 49 OF 76 SCISEARCH COPYRIGHT 2001 ISI (R)
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L85 ANSWER 50 OF 76 MEDLINE DUPLICATE 28
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that acute exposure to high cortisol levels is sufficient to induce the
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L85 ANSWER 51 OF 76 SCISEARCH COPYRIGHT 2001 ISI (R)
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L85 ANSWER 57 OF 76 EMBASE COPYRIGHT 2001 ELSEVIER SCI. B.V.DUPLICATE 31
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L85 ANSWER 58 OF 76 BIOSIS COPYRIGHT 2001 BIOSIS
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L85 ANSWER 65 OF 76 EMBASE COPYRIGHT 2001 ELSEVIER SCI. B.V.
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L85 ANSWER 68 OF 76 MEDLINE DUPLICATE 36
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AN 1974:459070 HCAPLUS
DN 81:59070

L85 ANSWER 76 OF 76 EMBASE COPYRIGHT 2001 ELSEVIER SCI. B.V.
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=> d ab 7,11,12,18,24,33,34,45,47,76

L85 ANSWER 7 OF 76 MEDLINE DUPLICATE 4
AB We used **sequence** motifs conserved in S-adenosylmethionine-
dependent methyltransferases to identify 26 putative methyltransferases
from the complete genome of the yeast *Saccharomyces cerevisiae*. Seven
sequences with the best matches to the methyltransferase consensus
motifs were selected for further study. We prepared yeast disruption
mutants of each of the **genes** encoding these **sequences**,
and we found that disruption of the YJL125c **gene** is lethal,
whereas disruptions of YCR047c and YDR140w lead to slow growth phenotypes.
Normal growth was observed when the YDL201w, YDR465c, YHR209w, and YOR240w
genes were disrupted. Initial analysis of protein methylation
patterns of all mutants by amino acid analysis revealed that the YDR465c
mutant has a defect in the methylation of the delta-nitrogen atom of
arginine residues. We propose that YDR465c codes for the methyltransferase
responsible for this recently characterized type of protein methylation,
and we designate the enzyme as Rmt2 (protein **arginine
methyltransferase**). In addition, we show that the methylation of
susceptible residues in Rmt2 substrates is likely to take place on nascent
polypeptide chains and that these substrates exist in the cell as fully
methylated species. Interestingly, Rmt2 has 27% **sequence**
identity over 138 amino acids to the mammalian guanidinoacetate
N-methyltransferase, an enzyme responsible for methylating the
delta-nitrogen of the small molecule guanidinoacetate.

L85 ANSWER 11 OF 76 MEDLINE DUPLICATE 5
AB Hrp1p is a heterogeneous ribonucleoprotein (hnRNP) from the yeast
Saccharomyces cerevisiae that is involved in the cleavage and
polyadenylation of the 3'-end of mRNAs and mRNA export. In addition, Hrp1p
is one of several RNA-binding proteins that are posttranslationally
modified by methylation at arginine residues. By using functional
recombinant Hrp1p, we have identified RNA **sequences** with
specific high affinity binding sites. These sites correspond to the
efficiency element for mRNA 3'-end formation, UAUUA. To examine the
effect of methylation on specific RNA binding, purified recombinant
arginine methyltransferase (Hmt1p) was used to methylate
Hrp1p. Methylated Hrp1p binds with the same affinity to UAUUA-containing
RNAs as unmethylated Hrp1p indicating that methylation does not affect
specific RNA binding. However, RNA itself inhibits the methylation of
Hrp1p and this inhibition is enhanced by RNAs that specifically bind Hrp1p.
Taken together, these data support a model in which protein methylation
occurs prior to protein-RNA binding in the nucleus.

L85 ANSWER 12 OF 76 SCISEARCH COPYRIGHT 2001 ISI (R)

L85 ANSWER 18 OF 76 EMBASE COPYRIGHT 2001 ELSEVIER SCI. B.V. DUPLICATE 9

AB Recombinant TIS21 protein was overexpressed in Escherichia coli harboring the expression vector plasmid pQE-30 carrying the TIS21 cDNA coding **sequence** containing an extra 120 nucleotides upstream. Employing this protein consisting of 158 amino acid residues of the main chain plus 40 residues of the fusion peptide, it was found that one of the protein methylase I group [S-adenosylmethionine:nuclear protein/histone-arginine N-methyltransferase; EC 2.1.1.23] methylated this protein. The methylation products were identified as guanidino-N-methylated arginines. Some of the kinetics of the reaction are described.

L85 ANSWER 24 OF 76 HCAPLUS COPYRIGHT 2001 ACS

AB This review, with 250 refs., summarizes the current status of protein arginine N-methylation reactions. These covalent modifications of proteins are now recognized in a no. of eukaryotic proteins and their functional significance is beginning to be understood. **Genes** that encode those methyltransferases specific for catalyzing the formation of asym. dimethylarginine have been identified. The enzyme modifies a no. of generally nuclear or nucleolar proteins that interact with nucleic acids, particularly RNA. Postulated roles for these reactions include signal transduction, nuclear transport, or a direct modulation of nucleic acid interactions. A second methyltransferase activity that sym. dimethylates an arginine residue in myelin basic protein, a major component of the axon sheath, has also been characterized. However, a **gene** encoding this activity has not been identified to date and the cellular function for this methylation reaction has not been clearly established. From the anal. of the **sequences** surrounding known arginine methylation sites, we have detd. consensus methyl-accepting **sequences** that may be useful in identifying novel substrates for these enzymes and may shed further light on their physiol. role. (c) 1998 Academic Press.

L85 ANSWER 33 OF 76 MEDLINE DUPLICATE 18

AB The intracytoplasmic domain (IC) of cytokine receptors provides docking sites for proteins which mediate signal transduction. Thus, in interferon-alpha,beta receptors (IFNAR1 and 2), the IC region binds protein-tyrosine and -serine/threonine kinases which phosphorylate the receptor and the associated Stat transcription factors. A two-hybrid screening was carried out to identify additional proteins which could interact with the IC domain of the IFNAR1 chain of the IFN-alpha,beta receptor. Several positive clones representing a protein **sequence** designated IR1B4 were recovered from a human cDNA library. IR1B4 was identified as the human homolog of PRMT1, a protein-**arginine methyltransferase** from rat cells. Flag-IR1B4 fusion proteins bind to the isolated IFNAR1 intracytoplasmic domain produced in Escherichia coli, as well as to the intact IFNAR1 chain extracted by detergent from human U266 cell membranes. S-Adenosylmethionine-dependent methyltransferase activity was precipitated by anti-IFNAR1 antibodies from untreated human cells. IR1B4/PRMT1 is involved in IFN action since U266 cells rendered deficient in this methyltransferase by antisense oligonucleotides become more resistant to growth inhibition by IFN. Methylation of proteins by enzymes which can attach to the IC domains of receptors may be a signaling mechanism complementing protein phosphorylation. Among substrates methylated by PRMT1 are RNA-binding heterogeneous nuclear ribonucleoproteins (hnRNPs) which are involved in mRNA processing, splicing and transport into the cytoplasm.

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DUPLICATE 19

AB The TIS21 immediate-early **gene** and leukemia-associated BTG1 **gene** encode proteins with similar **sequences**. Two-hybrid analysis identified a protein that interacts with TIS21 and BTG1. **Sequence** motifs associated with S-adenosyl-L-methionine binding suggested this protein might have methyltransferase activity. A glutathione S-transferase (GST) fusion of the putative methyltransferase modifies arginine residues, in appropriate protein substrates, to form NG-monomethyl and NG,NG-dimethylarginine (asymmetric). We term the protein- arginine N-methyltransferase (EC 2.1.1.23) **gene** "PRMT1, " for protein-**arginine methyltransferase 1**. GST-TIS21 and GST-BTG1 fusion proteins qualitatively and quantitatively modulate endogenous PRMT1 activity, using control and hypomethylated RAT1 cell extracts as methyl-accepting substrates. PRMT1 message appears ubiquitous, and is constitutive in mitogen-stimulated cells. Modulation of PRMT1 activity by transiently expressed regulatory subunits may be an additional mode of signal transduction following ligand stimulation.

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AB The enzymatic methylation of polypeptides on the guanidino group of internal arginine residues by S-adenosylmethionine:protein arginine N-methyltransferase (protein methylase I) yields N(G)-monomethylarginine, N(G),N(G)-dimethylarginine and N(G),N'(G)-dimethylarginine. It has commonly been observed that these arginine residues are present in glycine-and-arginine rich motifs. To understand structural features which are essential for serving as the methyl acceptor for protein methylase I, we have investigated substrate capacities of several synthetic oligopeptides whose **sequences** are homologous and/or analogous to the methyl acceptor region of the naturally occurring arginine-methylated proteins. These studies have led to the following conclusions. (i) The preferred amino-acid **sequence** of methyl-accepting peptides was shown to be an arginine-containing peptide with glycine in both the N- and C-flanking positions. While a tetrapeptide with such a **sequence** (residues 106-109 of bovine myelin basic protein) exhibited almost negligible substrate activity, an overlapping hexapeptide was a moderate substrate. (ii) Substitution of the C-flanking glycine in GKGRGL (residues 104-109 of myelin basic protein) with histidine, phenylalanine, lysine or aspartic acid completely abolished the ability of these hexapeptides to serve as substrates. (iii) A heptapeptide with a repeated glycine-arginine motif (GRGRGRG) was an excellent substrate for the enzyme. (iv) A cyclic octapeptide CGKGRGLC, which was formed by cyclization of GKGRGL by introduction of disulfide bridge to cross-link N- and C-terminus of the hexapeptide, was an even better substrate than the hexapeptide. (v) Upon HPLC amino-acid analysis, all enzymatically methyl-14C-labeled oligopeptides were found to yield predominantly N(G)-monomethylarginine with a minor fraction of N(G),N(G)-dimethylarginine in certain peptide samples. However, no N(G),N'(G)-dimethylarginine formation was detectable. (vi) The recombinant hnRNP protein A1 (residues 1-320) is known to be methylated at arginine-194 by nuclear-protein/histone protein methylase I (Rajpurohit et al. (1994) J. Biol. Chem. 269, 1079-1082). However, the hexapeptide (SSSQRG) which corresponds to residues 189-194 of protein A1 containing the methylatable arginine residue was relatively inert as a substrate. Furthermore, the N-terminal fragment of protein A1 (residues 1-196) generated by controlled trypsin digestion was also completely inactive as a substrate for the enzyme. These results indicate that the remainder of the A1 protein molecule plays an important though not yet understood role in enzymatic methylation of the arginine-194.

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DUPLICATE 27

AB Several proteins that interact with RNA, e.g. the heterogenous ribonucleoprotein particle A and B proteins, fibrillarin and nucleolin, contain the modified amino acid NG,NG-dimethylarginine. Here, we report that two synthetic peptides, Ac-GGRGGFGGRGGFGGRGGFG-NH₂ (R3) and GGFGRGGFG-NH₂ (R1), which are based on methylated **sequences** in fibrillarin and nucleolin, inhibit the methylation of a large majority of the methyl-accepting proteins observed in extracts of adenosine dialdehyde-treated PC12 cells. Concomitantly, the peptides themselves become methylated, suggesting that they compete for the same enzyme that carries out the bulk of N-methylation in PC12 cells. R3 potentially inhibits formation of NG,NG-dimethylarginine in PC12 substrates, with a lesser effect on NG-monomethylarginine and NG,N'-G-dimethylarginine. Bovine brain contains an activity that methylates PC12 methyl acceptors. After partial purification, the bovine methyltransferase efficiently modifies R3 and R1, yielding half maximal rates of methylation at approximately 0.2 and approximately 2 microM peptide, respectively. A search of the GenPept database for the FGGRGGF motif revealed 13 candidate methyl acceptors containing arginine and at most two similar substitutions or one mismatch. Of these, 10 are known or presumed to interact with RNA. These findings are consistent with the hypothesis that a majority of proteins containing NG,NG-dimethylarginine interact with RNA.

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AB S Adenosyl L ethionine was found to inhibit histone methylation by an **arginine methyltransferase** purified from rat liver cytoplasm, in the presence of S adenosyl L methionine. The enzyme is able to transfer alkyl groups from either of the activated amino acids to histone and with comparable efficiency. Histone methylation is also inhibited by N hydroxy 2 acetylaminofluorene (40% at 1 mM inhibitor concentration) and N acetoxy 2 acetylaminofluorene (69% at 1.0 mM inhibitor concentration). The **arginine methyltransferase** has a Km value of 4.4 .mu.M and is subject to product inhibition by S adenosyl L homocysteine (Ki = 1.2 .mu.M). Other similarities to the transfer ribonucleic acid methyltransferases are susceptibility to inhibition by adenine and the adenosine analogs, tubercidin and N 6 (.DELTA.2 isopentenyl) adenosine (16, 79, and 72%, respectively, at 1.0 mM inhibitor concentrations). The dyes ethidium bromide and acridine orange also inhibit the methyltransferase system (58 and 80%, respectively, at 1.0 mM inhibitor concentrations). The observation that arginine methylation in histones is inhibited by reactive metabolites of carcinogenic agents is used as a basis for proposing that interference in the normal histone methylation process, with resultant effects on fidelity of **gene** expression represents a preliminary step in carcinogenesis by such agents.

=> log y

COST IN U.S. DOLLARS

SINCE FILE	TOTAL
ENTRY	SESSION
40.18	165.11

FULL ESTIMATED COST

DISCOUNT AMOUNTS (FOR QUALIFYING ACCOUNTS)

SINCE FILE	TOTAL
ENTRY	SESSION
-0.59	-0.59

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